

OM nucleic - nucleic search, using sw model

Run on: February 14, 2005, 22:56:12 ; Search time 9798 Seconds
(without alignments)
12210.247 Million cell updates/sec

Title: US-10-015-391A-276
Perfect score: 3143
Sequence: 1 gggctgaggcactgagagac.....aaatataaggcttaaaaaaa 3143

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gssl:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3005	95.6	3005	3	CR623694	CR623694 full-leng
2	2927.6	93.1	3151	3	HSM807023	BX640891 Homo sapi
3	1874	59.6	2172	9	AY402621	AY402621 Homo sapi
4	1765.4	56.2	2133	9	AY402622	AY402622 Pan trogl
5	1747.4	55.6	3206	3	AK077976	AK077976 Mus muscu
6	1701.4	54.1	3086	3	AK035918	AK035918 Mus muscu
7	1372.2	43.7	2172	9	AY402623	AY402623 Mus muscu
c 8	950.6	30.2	1108	5	BX367242	BX367242 BX367242

c	9	926.2	29.5	1064	5	BX363741	BX363741	BX363741
c	10	874.4	27.8	922	5	BX350606	BX350606	BX350606
	11	849.2	27.0	934	5	BX384966	BX384966	BX384966
	12	839	26.7	897	5	BX328255	BX328255	BX328255
	13	827.4	26.3	974	5	BQ057192	BQ057192	AGENCOURT
	14	820.4	26.1	944	5	BX390196	BX390196	BX390196
c	15	779.8	24.8	797	6	CB243787	CB243787	UI-CF-FN0
	16	775	24.7	801	5	BX112994	BX112994	BX112994
	17	769.8	24.5	912	5	BQ883972	BQ883972	AGENCOURT
	18	768	24.4	958	5	BX376660	BX376660	BX376660
	19	757.6	24.1	892	6	CD107028	CD107028	AGENCOURT
c	20	756.2	24.1	819	6	CD631371	CD631371	56050427H
	21	748.6	23.8	951	5	BQ056228	BQ056228	AGENCOURT
	22	696.6	22.2	775	1	AU122156	AU122156	AU122156
	23	691.2	22.0	970	5	BQ707628	BQ707628	AGENCOURT
	24	681	21.7	1066	4	BM806752	BM806752	AGENCOURT
c	25	675.2	21.5	763	6	CD631373	CD631373	56066030H
	26	674	21.4	727	7	CN255817	CN255817	170004252
	27	673	21.4	960	5	BX367243	BX367243	BX367243
	28	666	21.2	706	6	CD631372	CD631372	56050427J
	29	664	21.1	681	7	CV023527	CV023527	490 Full
	30	661.8	21.1	666	4	BG684636	BG684636	602635914
	31	650	20.7	925	5	BQ937439	BQ937439	AGENCOURT
c	32	627.4	20.0	640	6	CA311774	CA311774	UI-CF-FN0
c	33	612	19.5	624	4	BM666780	BM666780	UI-E-CL1-
	34	609.8	19.4	1119	4	BI550650	BI550650	603195823
	35	608.4	19.4	803	7	CN539797	CN539797	UI-M-HU0-
	36	598.6	19.0	621	2	AW965845	AW965845	EST377918
c	37	598.4	19.0	634	5	BU632880	BU632880	UI-H-FE1-
c	38	594	18.9	618	5	BU686374	BU686374	UI-CF-DU1
	39	590.8	18.8	740	6	CD631374	CD631374	56066030J
	40	585.2	18.6	881	5	BQ960065	BQ960065	AGENCOURT
	41	579.2	18.4	720	6	CA315771	CA315771	UI-M-FW0-
	42	579	18.4	580	5	BP346261	BP346261	BP346261
	43	576.2	18.3	582	5	BP312448	BP312448	BP312448
	44	568.6	18.1	783	7	CK483764	CK483764	AGENCOURT
	45	566.8	18.0	582	5	BP305311	BP305311	BP305311
	46	565.8	18.0	571	7	CR554650	CR554650	DKFZp4590
	47	557.8	17.7	796	5	BU052878	BU052878	UI-M-FC0-
	48	554.4	17.6	718	7	CK837783	CK837783	4063044 B
	49	552.6	17.6	917	6	CA454892	CA454892	AGENCOURT
	50	552.4	17.6	779	4	BI683727	BI683727	603306287
	51	551.4	17.5	695	4	BG685741	BG685741	602637838
	52	547	17.4	547	4	BM128651	BM128651	if14b09.y
	53	546.6	17.4	709	5	BQ573544	BQ573544	UI-M-FD0-
	54	542.6	17.3	667	4	BG703963	BG703963	602687061
	55	542.2	17.3	784	5	BQ043061	BQ043061	UI-M-EG0p
	56	538.6	17.1	841	6	CB566426	CB566426	AGENCOURT
	57	530	16.9	550	5	BP292524	BP292524	BP292524
	58	528	16.8	528	6	CA393520	CA393520	cs39b03.y
	59	526.2	16.7	944	4	BI250501	BI250501	602993551
	60	524.4	16.7	858	7	CK022938	CK022938	AGENCOURT
c	61	522.4	16.6	536	5	BQ356019	BQ356019	PM3-HT130
	62	510.8	16.3	793	4	BI146386	BI146386	602910749
	63	510	16.2	666	2	BE868099	BE868099	601443414
	64	507.8	16.2	519	7	CK819350	CK819350	if14b09.y
	65	500.2	15.9	532	4	BM691378	BM691378	UI-E-CI1-

	66	500.2	15.9	758	4	BI105301	BI105301	602893591
c	67	498	15.8	567	1	AU147813	AU147813	AU147813
	68	495.4	15.8	628	7	CN792080	CN792080	4126901 B
	69	494	15.7	598	2	BE588408	BE588408	194035 BA
	70	486.6	15.5	788	7	CK481778	CK481778	AGENCOURT
	71	486	15.5	969	4	BG247839	BG247839	602359548
	72	481.6	15.3	632	7	CK625364	CK625364	mi32c08.y
	73	481	15.3	481	4	BM694992	BM694992	UI-E-CL1-
c	74	478.8	15.2	503	1	AI817099	AI817099	wj76h11.x
	75	478.8	15.2	810	6	CB587284	CB587284	AGENCOURT
	76	476.8	15.2	544	4	BI481387	BI481387	H2RPE-174
	77	470.4	15.0	530	1	AA481246	AA481246	aa34h11.r
c	78	469.2	14.9	562	2	AW836429	AW836429	PM3-LT003
	79	467.8	14.9	821	5	BQ442696	BQ442696	UI-M-EV0-
	80	465.4	14.8	806	7	CK481746	CK481746	AGENCOURT
	81	464.6	14.8	585	4	BI359871	BI359871	384615 MA
	82	462.6	14.7	667	2	AW914963	AW914963	EST346267
	83	462.2	14.7	887	4	BI219079	BI219079	602938695
	84	461.4	14.7	672	6	BY747595	BY747595	BY747595
	85	461.2	14.7	892	5	BQ934892	BQ934892	AGENCOURT
	86	449.6	14.3	537	2	AW657913	AW657913	93554 MAR
	87	447	14.2	872	4	BI150290	BI150290	602915311
c	88	446.4	14.2	450	1	AI568200	AI568200	tn66h01.x
	89	444	14.1	822	7	CO565372	CO565372	AGENCOURT
	90	443.8	14.1	659	6	BY747925	BY747925	BY747925
c	91	443.4	14.1	456	5	BU726485	BU726485	UI-E-CI1-
c	92	442.4	14.1	444	5	BQ356020	BQ356020	PM3-HT130
c	93	440.6	14.0	468	5	BQ356018	BQ356018	PM3-HT130
	94	439.6	14.0	578	4	BI341318	BI341318	368709 MA
c	95	436.8	13.9	440	1	AA973640	AA973640	oo48c04.s
	96	435.2	13.8	579	4	BI360284	BI360284	387146 MA
	97	432.4	13.8	621	9	CG591258	CG591258	OST245642
	98	431	13.7	632	7	CO581119	CO581119	ILLUMIGEN
	99	430.8	13.7	794	2	BF578994	BF578994	602096109
	100	427	13.6	563	4	BM030859	BM030859	495387 MA
c	101	426.8	13.6	441	1	AA554541	AA554541	nl14b01.s
	102	426.8	13.6	827	7	CO404310	CO404310	AGENCOURT
	103	425.2	13.5	443	2	BF882612	BF882612	QV3-ET020
c	104	425.2	13.5	457	1	AI291110	AI291110	qml0d09.x
	105	422.8	13.5	546	2	BF199358	BF199358	249500 MA
	106	422.4	13.4	759	4	BG243769	BG243769	602357081
	107	418.4	13.3	576	4	BI345630	BI345630	374508 MA
c	108	415	13.2	415	1	AI017230	AI017230	ou32d12.x
	109	415	13.2	536	2	BF199378	BF199378	249524 MA
c	110	414.6	13.2	454	2	BF882611	BF882611	QV3-ET020
	111	414.6	13.2	538	2	BF080018	BF080018	230753 MA
c	112	413.6	13.2	537	5	BX372943	BX372943	BX372943
	113	413	13.1	583	5	BP315573	BP315573	BP315573
c	114	412.6	13.1	468	7	T34379	T34379	EST66750 Hu
	115	412	13.1	582	5	BP314196	BP314196	BP314196
	116	411	13.1	581	5	BP314893	BP314893	BP314893
	117	410.8	13.1	624	4	BM691301	BM691301	UI-E-CI1-
	118	409	13.0	582	5	BP312657	BP312657	BP312657
	119	409	13.0	721	2	BF580373	BF580373	602097124
	120	408	13.0	473	7	H08023	H08023	yl91d06.r1
	121	406	12.9	406	7	CR538178	CR538178	DKFZp459F
	122	405	12.9	583	5	BP314892	BP314892	BP314892

123	404.8	12.9	870	2	BE306403	BE306403	601102295
124	404.6	12.9	610	4	BG618720	BG618720	602645175
125	403.2	12.8	1122	2	BF159534	BF159534	601769029
c 126	402.6	12.8	449	1	AI623385	AI623385	ts18g03.x
127	401.4	12.8	581	5	BP357544	BP357544	BP357544
128	395.4	12.6	634	1	AA646591	AA646591	ve46d08.r
129	394.8	12.6	494	4	BM288077	BM288077	528964 MA
130	392.4	12.5	766	7	CK478839	CK478839	AGENCOURT
131	392.2	12.5	882	2	BE571537	BE571537	601333983
132	392	12.5	582	5	BP315572	BP315572	BP315572
133	391.6	12.5	555	6	CB613565	CB613565	AMGNNUC:N
134	390.6	12.4	581	6	CB606887	CB606887	AMGNNUC:N
135	388.8	12.4	465	2	BF882607	BF882607	QV3-ET020
136	388	12.3	618	6	CB579294	CB579294	AMGNNUC:N
137	387.4	12.3	544	4	BI961174	BI961174	MONO1_7_A
c 138	387	12.3	405	1	AI221749	AI221749	qq93f04.x
139	383	12.2	713	6	BY763638	BY763638	BY763638
c 140	380.8	12.1	412	1	AA761091	AA761091	ny13g11.s
141	378	12.0	598	1	AV617761	AV617761	AV617761
142	377.4	12.0	535	5	BQ552175	BQ552175	H4013H07-
143	377.2	12.0	665	4	BI151295	BI151295	602917272
c 144	374.4	11.9	459	2	BF154829	BF154829	PM2-BT076
c 145	374.4	11.9	459	4	BG949399	BG949399	PM2-BT076
146	372.4	11.8	582	5	BP314933	BP314933	BP314933
147	370.6	11.8	600	6	CA530364	CA530364	9034-81 M
148	370.2	11.8	541	2	AW654459	AW654459	103930 MA
c 149	369.4	11.8	464	5	BQ356179	BQ356179	PM3-HT130
150	367.4	11.7	490	2	AW659681	AW659681	97213 MAR
151	367	11.7	516	2	BF075002	BF075002	223731 MA
c 152	366.4	11.7	369	2	AW593031	AW593031	hg07e10.x
153	363.8	11.6	368	1	AA419534	AA419534	zv03c09.r
154	363.4	11.6	513	4	BM106299	BM106299	509997 MA
155	360.6	11.5	742	6	CB249229	CB249229	UI-M-FC0-
156	356.4	11.3	583	5	BP357148	BP357148	BP357148
157	355	11.3	529	5	BU698229	BU698229	LL2in1365
c 158	354.4	11.3	363	1	AI221756	AI221756	qq93f12.x
159	353	11.2	576	4	BI914790	BI914790	603184176
c 160	351.4	11.2	737	7	CO425778	CO425778	UI-M-HU0-
161	348	11.1	360	7	T19441	T19441	f03002s Tes
c 162	346	11.0	358	1	AI682007	AI682007	tp45g08.x
163	344.8	11.0	502	5	BU696522	BU696522	LL2in1072
164	344.2	11.0	623	2	BB628588	BB628588	BB628588
165	343.6	10.9	424	2	AW352877	AW352877	35717 MAR
166	340.4	10.8	552	2	AW655294	AW655294	106095 MA
167	338.6	10.8	449	5	BQ336149	BQ336149	PM0-MT042
168	337.2	10.7	545	2	AW654538	AW654538	104068 MA
169	334.8	10.7	479	4	BM088355	BM088355	501805 MA
170	333.2	10.6	411	2	BE859656	BE859656	UI-M-AL0-
171	332.2	10.6	443	2	AW355069	AW355069	37338 MAR
172	327.4	10.4	700	5	BM944176	BM944176	UI-M-EH0p
c 173	326.8	10.4	330	7	CK819349	CK819349	if14b09.x
174	321.8	10.2	469	1	AJ650325	AJ650325	AJ650325
175	321.2	10.2	445	2	AW481698	AW481698	37332 MAR
176	320.6	10.2	433	2	AW355070	AW355070	37337 MAR
177	318.6	10.1	390	6	CB778065	CB778065	AMGNNUC:C
178	318.4	10.1	432	2	BF019645	BF019645	ux14b02.y
c 179	316.8	10.1	353	2	AW628784	AW628784	hi39e03.x

	180	316.2	10.1	465	7	R81743	R81743 yj05d01.r1
c	181	315.8	10.0	469	1	AI141990	AI141990 ool7g10.x
	182	312.4	9.9	443	4	BM106612	BM106612 510531 MA
c	183	310.6	9.9	346	5	BQ335891	BQ335891 PM3-MT020
c	184	310	9.9	356	2	AW298440	AW298440 UI-H-BW0-
c	185	308.4	9.8	310	1	AA687813	AA687813 nv12e08.s
c	186	308	9.8	456	7	CV374906	CV374906 PM3-HT130
	187	302.6	9.6	514	1	AA959087	AA959087 ua08f08.r
	188	302	9.6	388	6	CB779567	CB779567 AMGNNUC:N
	189	301	9.6	582	5	BP250593	BP250593 BP250593
	190	299.8	9.5	717	5	BM946956	BM946956 UI-M-EH0p
	191	298.6	9.5	583	5	BU694619	BU694619 LL2in1402
	192	298.4	9.5	437	2	BF605420	BF605420 271789 MA
	193	293.6	9.3	435	6	BY596404	BY596404 BY596404
	194	293.6	9.3	480	6	CB537061	CB537061 772134 MA
	195	293.6	9.3	512	1	AA510439	AA510439 vg32e04.r
c	196	293.2	9.3	303	7	T19440	T19440 f03002t Tes
	197	293	9.3	439	4	BM030747	BM030747 495245 MA
	198	289.6	9.2	689	1	AA274712	AA274712 vc15g11.r
	199	288.8	9.2	318	2	BE182018	BE182018 CM1-HT064
	200	288.2	9.2	368	2	AW632286	AW632286 92080 MAR
	201	287.6	9.2	655	2	BB621440	BB621440 BB621440
	202	287.2	9.1	475	4	BM286849	BM286849 527060 MA
	203	286.6	9.1	418	6	CB765926	CB765926 AMGNNUC:N
c	204	286.4	9.1	298	4	BM662404	BM662404 UI-E-CI1-
	205	285.8	9.1	481	7	W13797	W13797 ma94g12.r1
	206	285.8	9.1	514	9	CG646708	CG646708 OST393408
	207	285.6	9.1	354	2	BE155671	BE155671 PM2-HT035
	208	284.4	9.0	286	7	CN255816	CN255816 170005325
	209	283.6	9.0	398	2	BE014053	BE014053 125627 MA
	210	280.6	8.9	532	1	AA575453	AA575453 vl90b06.r
	211	279.4	8.9	285	7	CR736197	CR736197 CR736197
	212	279	8.9	512	2	BE012711	BE012711 122368 MA
c	213	273.6	8.7	343	7	R81500	R81500 yj05d01.s1
c	214	273.4	8.7	281	7	Z39973	Z39973 HSC10E102 n
	215	273	8.7	736	2	BE288736	BE288736 601093420
	216	271.4	8.6	327	7	Z43916	Z43916 HSC10E101 n
	217	269.4	8.6	636	6	BY745271	BY745271 BY745271
	218	261.6	8.3	385	6	CB702615	CB702615 AMGNNUC:S
	219	261.2	8.3	338	1	AA193482	AA193482 zr41d02.r
	220	257.4	8.2	507	2	BE668290	BE668290 156950 MA
	221	257.2	8.2	456	2	BB840212	BB840212 BB840212
	222	255	8.1	307	7	T34380	T34380 EST66751 Hu
	223	253	8.0	595	7	CN701121	CN701121 E0445B08-
	224	248.8	7.9	2480	9	AY407393	AY407393 Mus muscu
	225	248.6	7.9	343	2	AW446374	AW446374 85396 MAR
	226	247.8	7.9	407	5	BY201059	BY201059 BY201059
	227	247.4	7.9	339	7	CK942886	CK942886 4066584 B
	228	247.2	7.9	415	5	BY237094	BY237094 BY237094
	229	244	7.8	731	1	AI116589	AI116589 ue27f05.y
c	230	241.4	7.7	528	1	AI350408	AI350408 qt17b12.x
	231	241	7.7	330	2	AW483617	AW483617 55275 MAR
	232	240.6	7.7	3809	3	AK030331	AK030331 Mus muscu
	233	239	7.6	2777	3	AK028896	AK028896 Mus muscu
	234	234.8	7.5	548	5	BX515711	BX515711 BX515711
	235	233.6	7.4	517	2	BB867776	BB867776 BB867776
	236	233.2	7.4	359	5	BY344631	BY344631 BY344631

	237	233	7.4	529	1	AI119178	AI119178	ue23g10.y
c	238	232.2	7.4	259	1	AI698802	AI698802	wd31b11.x
	239	229.4	7.3	352	5	BY209243	BY209243	BY209243
	240	229.4	7.3	353	5	BY194675	BY194675	BY194675
	241	228.2	7.3	345	6	CB705908	CB705908	AMGNNUC:N
	242	227.6	7.2	2502	9	AY407391	AY407391	Homo sapi
	243	226.2	7.2	359	5	BY192032	BY192032	BY192032
	244	225.8	7.2	441	2	BB848500	BB848500	BB848500
	245	222.8	7.1	354	5	BY186467	BY186467	BY186467
c	246	222	7.1	226	1	AA971074	AA971074	op70g02.s
	247	220.6	7.0	399	5	BY258404	BY258404	BY258404
c	248	218.4	6.9	231	1	AA588098	AA588098	nm98h03.s
	249	218.4	6.9	356	5	BY203094	BY203094	BY203094
c	250	216.2	6.9	224	1	AA481169	AA481169	aa34h11.s
	251	216.2	6.9	555	7	CN699228	CN699228	E0418E11-
	252	216.2	6.9	925	5	BQ929233	BQ929233	AGENCOURT
	253	215.4	6.9	787	4	BI665818	BI665818	603289737
	254	213.4	6.8	978	5	BQ219389	BQ219389	AGENCOURT
	255	213.2	6.8	766	4	BI330594	BI330594	602981035
	256	212.8	6.8	344	5	BY182086	BY182086	BY182086
	257	212.4	6.8	342	5	BY190812	BY190812	BY190812
	258	212	6.7	554	1	AL780781	AL780781	AL780781
	259	211	6.7	3648	3	AK090073	AK090073	Mus muscu
	260	210.6	6.7	360	5	BY203098	BY203098	BY203098
	261	210	6.7	350	9	CG604636	CG604636	OST280536
	262	202.8	6.5	906	7	CF548431	CF548431	AGENCOURT
	263	201.6	6.4	361	6	BY780664	BY780664	BY780664
	264	199.4	6.3	340	5	BY180833	BY180833	BY180833
	265	198	6.3	904	2	BF134543	BF134543	601784950
	266	196.8	6.3	343	5	BY176481	BY176481	BY176481
	267	194.2	6.2	457	5	BY225325	BY225325	BY225325
	268	192	6.1	374	6	CB692309	CB692309	AMGNNUC:N
	269	191.8	6.1	398	5	BY284987	BY284987	BY284987
	270	191.6	6.1	691	7	CF767810	CF767810	CES006164
	271	190.6	6.1	298	2	BB586510	BB586510	BB586510
	272	190.4	6.1	380	5	BY265162	BY265162	BY265162
	273	189.8	6.0	424	5	BY188709	BY188709	BY188709
	274	189	6.0	386	5	BY231195	BY231195	BY231195
	275	186.6	5.9	267	4	BM485185	BM485185	539436 MA
	276	185.4	5.9	2502	9	AY407392	AY407392	Pan trogl
c	277	184.6	5.9	588	6	CB469303	CB469303	sn05_G02.
	278	181	5.8	504	2	BE481474	BE481474	166929 BA
	279	179.2	5.7	838	7	CF374334	CF374334	AGENCOURT
	280	176.4	5.6	416	5	BY183408	BY183408	BY183408
c	281	176	5.6	560	6	CB476226	CB476226	jns118_A0
	282	172.8	5.5	710	6	CB422627	CB422627	595748 MA
	283	170	5.4	312	5	BY170795	BY170795	BY170795
	284	169.2	5.4	782	5	BP684334	BP684334	BP684334
	285	166.8	5.3	297	5	BY000550	BY000550	BY000550
	286	165.8	5.3	356	5	BY233307	BY233307	BY233307
	287	163	5.2	411	6	BY547048	BY547048	BY547048
	288	163	5.2	437	7	CV312033	CV312033	CM0-PT004
	289	161.4	5.1	768	5	BM943605	BM943605	UI-M-EH0p
c	290	160.4	5.1	299	5	BQ356197	BQ356197	PM3-HT130
	291	158.2	5.0	724	4	BG716692	BG716692	602678071
	292	157	5.0	902	5	BQ933408	BQ933408	AGENCOURT
c	293	154.8	4.9	571	6	CB438091	CB438091	686532 MA

	294	154.6	4.9	473	4	BI775884	BI775884	468605	MA
	295	153.8	4.9	164	7	D45630	D45630	HUMGS02826	
c	296	153.8	4.9	626	6	CB431656	CB431656	607652	MA
c	297	153.6	4.9	582	6	CB535123	CB535123	768510	MA
	298	153.2	4.9	863	1	AI323192	AI323192	mp55g10.y	
	299	152	4.8	745	5	BM962964	BM962964	UI-M-EQ0-	
c	300	151.6	4.8	172	2	AW467911	AW467911	he28c12.x	
	301	150.2	4.8	780	7	CN255480	CN255480	170005312	
	302	149.8	4.8	615	1	AL677440	AL677440	AL677440	
	303	149	4.7	834	5	BQ216757	BQ216757	AGENCOURT	
	304	146.4	4.7	977	5	BX370082	BX370082	BX370082	
	305	146	4.6	211	4	BI345631	BI345631	374509	MA
	306	146	4.6	886	5	BQ943608	BQ943608	AGENCOURT	
	307	145.8	4.6	448	2	BB847529	BB847529	BB847529	
	308	145	4.6	416	2	AW430454	AW430454	70020	MAR
	309	143.8	4.6	615	6	CB437039	CB437039	684474	MA
	310	143.6	4.6	175	2	AW313646	AW313646	9051	MARC
	311	141.8	4.5	1068	4	BM811543	BM811543	AGENCOURT	
	312	141.4	4.5	926	5	BU909663	BU909663	AGENCOURT	
	313	141	4.5	706	7	CN255488	CN255488	170006001	
	314	141	4.5	728	7	CN255483	CN255483	170005322	
	315	141	4.5	864	4	BI518922	BI518922	603061844	
	316	140	4.5	270	2	BB608272	BB608272	BB608272	
	317	140	4.5	568	7	CN255489	CN255489	170005322	
	318	136.8	4.4	443	5	BY167445	BY167445	BY167445	
	319	136.4	4.3	580	2	BE752387	BE752387	204762	MA
	320	134	4.3	160	7	CO261051	CO261051	4133142	B
	321	134	4.3	948	5	BQ685036	BQ685036	AGENCOURT	
	322	133	4.2	770	7	CO248318	CO248318	AGENCOURT	
c	323	132.2	4.2	573	2	AW118237	AW118237	xe12b08.x	
c	324	131.4	4.2	467	1	AV617760	AV617760	AV617760	
	325	131.4	4.2	615	5	BM945001	BM945001	UI-M-EH0p	
	326	130.4	4.1	563	6	CD216221	CD216221	pgp2n.pk0	
	327	130.4	4.1	700	1	AA763586	AA763586	vp07g05.r	
c	328	130	4.1	561	4	BM252112	BM252112	BOTL01000	
	329	129.8	4.1	614	4	BG712158	BG712158	pgl1n.pk0	
	330	129.6	4.1	418	2	BE679181	BE679181	dc60b02.y	
c	331	129.6	4.1	547	4	BM220500	BM220500	C0941F04-	
c	332	129.6	4.1	598	2	BF714461	BF714461	mab01a06.	
	333	129.6	4.1	700	6	BY763889	BY763889	BY763889	
c	334	129.6	4.1	711	5	BP765487	BP765487	BP765487	
c	335	129.6	4.1	773	1	AI132332	AI132332	ue23g10.x	
c	336	129.6	4.1	780	7	CO040927	CO040927	UI-M-EV0-	
	337	129.2	4.1	678	6	CA041134	CA041134	ssalshc50	
	338	129.2	4.1	3763	3	AK088653	AK088653	Mus muscu	
	339	128.8	4.1	708	7	CN789123	CN789123	4123542	B
	340	128.2	4.1	372	6	BY540732	BY540732	BY540732	
	341	128	4.1	674	2	BB045065	BB045065	BB045065	
	342	127.2	4.0	290	2	AW656129	AW656129	108203	MA
c	343	127	4.0	601	5	BP768508	BP768508	BP768508	
	344	126.8	4.0	625	2	BE077531	BE077531	RC1-BT060	
	345	126.6	4.0	342	1	AA611491	AA611491	vo89a05.r	
	346	126.6	4.0	403	6	BY540418	BY540418	BY540418	
	347	126.2	4.0	426	2	BB824296	BB824296	BB824296	
	348	126.2	4.0	435	5	BY517409	BY517409	BY517409	
	349	125.8	4.0	593	6	CD216085	CD216085	pgp2n.pk0	
	350	125.6	4.0	387	5	BY504344	BY504344	BY504344	

351	125.6	4.0	410	5	BY510171	BY510171	BY510171
352	125.6	4.0	422	5	BY494879	BY494879	BY494879
353	125.4	4.0	455	7	CN223958	CN223958	WLA052D09
354	125.2	4.0	306	2	AW436384	AW436384	76556 MAR
355	125.2	4.0	344	1	AA611501	AA611501	vo89b04.r
356	125.2	4.0	355	1	AA823216	AA823216	vw42b01.r
357	125.2	4.0	366	2	BB792067	BB792067	BB792067
c 358	125.2	4.0	386	5	BX639014	BX639014	BX639014
c 359	125.2	4.0	396	2	BE851923	BE851923	uw18f07.x
360	125.2	4.0	404	6	BY575062	BY575062	BY575062
361	125.2	4.0	405	6	BY625364	BY625364	BY625364
362	125.2	4.0	408	6	BY547045	BY547045	BY547045
363	125.2	4.0	409	2	BB743231	BB743231	BB743231
364	125.2	4.0	414	6	BY538798	BY538798	BY538798
365	125.2	4.0	428	6	BY579800	BY579800	BY579800
366	125.2	4.0	434	6	BY551281	BY551281	BY551281
367	125.2	4.0	437	6	BY523338	BY523338	BY523338
c 368	125.2	4.0	441	2	AW061291	AW061291	UI-M-BH1-
369	125.2	4.0	449	6	BY546162	BY546162	BY546162
370	125.2	4.0	466	2	BB731279	BB731279	BB731279
371	125.2	4.0	469	2	BB824926	BB824926	BB824926
372	125.2	4.0	492	2	AW493316	AW493316	UI-M-BH3-
c 373	125.2	4.0	507	2	AW060306	AW060306	UI-M-BH1-
c 374	125.2	4.0	514	2	BF020082	BF020082	ux14b02.x
c 375	125.2	4.0	516	1	AI098213	AI098213	ue27f05.x
c 376	125.2	4.0	546	1	AI323581	AI323581	mp55g10.x
377	125.2	4.0	910	5	BU552547	BU552547	AGENCOURT
378	124.8	4.0	768	7	CN255481	CN255481	170005331
379	124.4	4.0	372	5	BY236908	BY236908	BY236908
380	124.2	4.0	387	5	BY511124	BY511124	BY511124
381	124.2	4.0	685	6	CA371810	CA371810	652409 NC
382	124	3.9	396	6	BY548006	BY548006	BY548006
c 383	124	3.9	446	1	AI606228	AI606228	vn98f09.x
384	123.8	3.9	314	2	AW485003	AW485003	63380 MAR
385	123.8	3.9	862	5	BQ224734	BQ224734	AGENCOURT
386	123.6	3.9	399	6	BY541776	BY541776	BY541776
387	123.6	3.9	410	5	BY513291	BY513291	BY513291
388	123.6	3.9	433	5	BY498637	BY498637	BY498637
389	123.6	3.9	660	2	BB126942	BB126942	BB126942
390	123.6	3.9	853	7	CR574223	CR574223	CR574223
391	123.4	3.9	319	2	BB317324	BB317324	BB317324
392	123.2	3.9	406	5	BY516094	BY516094	BY516094
c 393	123.2	3.9	446	5	BP754487	BP754487	BP754487
394	123.2	3.9	655	4	BJ618310	BJ618310	BJ618310
395	123	3.9	330	2	BB164759	BB164759	BB164759
396	123	3.9	446	2	BB820315	BB820315	BB820315
397	122.8	3.9	236	2	BF776808	BF776808	288536 MA
398	122.8	3.9	851	7	CF243117	CF243117	AGENCOURT
399	122.8	3.9	880	5	BU541109	BU541109	AGENCOURT
400	122.6	3.9	399	6	BY658194	BY658194	BY658194
401	122.6	3.9	405	2	BB739127	BB739127	BB739127
402	122.6	3.9	414	2	BE849780	BE849780	uw18f07.y
403	122.6	3.9	417	5	BY516312	BY516312	BY516312
404	122.6	3.9	432	6	BY525070	BY525070	BY525070
405	122.6	3.9	445	2	BB779387	BB779387	BB779387
406	122.4	3.9	399	5	BY183603	BY183603	BY183603
407	122.4	3.9	401	5	BY507720	BY507720	BY507720

408	122.2	3.9	343	2	BB222788	BB222788	BB222788
409	122.2	3.9	415	6	BY646549	BY646549	BY646549
410	122.2	3.9	420	6	BY524914	BY524914	BY524914
c 411	122.2	3.9	515	4	BM390926	BM390926	UI-R-CN1-
412	122	3.9	347	2	BB113642	BB113642	BB113642
413	122	3.9	402	5	BY507653	BY507653	BY507653
414	121.8	3.9	314	1	AV235779	AV235779	AV235779
415	121.8	3.9	548	2	BF039888	BF039888	BP250025A
416	121.8	3.9	932	5	BX369159	BX369159	BX369159
417	121.6	3.9	623	4	BJ095128	BJ095128	BJ095128
418	121.6	3.9	881	4	BG824522	BG824522	602727494
c 419	121.4	3.9	651	4	BM385797	BM385797	UI-R-CN1-
420	121.2	3.9	358	5	BY205630	BY205630	BY205630
421	121.2	3.9	872	4	BG831590	BG831590	602765850
c 422	121	3.8	293	7	CO988317	CO988317	UMC-pd3en
c 423	121	3.8	387	2	BE690913	BE690913	uw60d09.x
424	120.8	3.8	336	2	BB219364	BB219364	BB219364
425	120.8	3.8	589	4	BI391274	BI391274	pgpln.pk0
426	120.6	3.8	351	2	BE668250	BE668250	156853 MA
c 427	120.6	3.8	431	6	CA945768	CA945768	UI-R-FS1-
c 428	120.6	3.8	435	1	AI454122	AI454122	UI-R-BT0-
c 429	120.6	3.8	473	2	AW523699	AW523699	UI-R-BO0-
c 430	120.6	3.8	552	2	BE110750	BE110750	UI-R-BJ1-
c 431	120.6	3.8	555	5	BQ190381	BQ190381	UI-R-DN1-
c 432	120.6	3.8	649	6	CB322846	CB322846	UI-R-DY0-
433	120.4	3.8	328	2	BB223967	BB223967	BB223967
434	120.4	3.8	377	6	BY630131	BY630131	BY630131
435	120.4	3.8	424	5	BY378169	BY378169	BY378169
c 436	120.4	3.8	528	5	BQ031863	BQ031863	UI-1-CF0-
c 437	120.2	3.8	381	7	CR468045	CR468045	CR468045
438	120.2	3.8	446	1	AA254731	AA254731	mz80h03.r
439	120.2	3.8	486	6	BY591764	BY591764	BY591764
c 440	120.2	3.8	656	4	BM251667	BM251667	BOTL01000
441	120	3.8	324	2	BB503600	BB503600	BB503600
442	120	3.8	904	5	BU543096	BU543096	AGENCOURT
443	119.8	3.8	317	2	BB828413	BB828413	BB828413
444	119.8	3.8	414	5	BY498892	BY498892	BY498892
445	119.4	3.8	325	2	BB392255	BB392255	BB392255
446	119.4	3.8	333	1	AA755192	AA755192	vq62b08.r
447	119.4	3.8	447	6	BY539681	BY539681	BY539681
448	119.2	3.8	329	2	BB321099	BB321099	BB321099
449	119.2	3.8	961	5	BU542955	BU542955	AGENCOURT
450	119	3.8	262	2	AW313948	AW313948	9649 MARC
451	119	3.8	262	2	AW477528	AW477528	13351 MAR
452	118.6	3.8	316	2	BB210291	BB210291	BB210291
453	118.4	3.8	422	5	BY509778	BY509778	BY509778
454	118.4	3.8	808	5	BU187281	BU187281	AGENCOURT
c 455	118.2	3.8	392	4	BI290997	BI290997	UI-R-DK0-
456	118.2	3.8	670	7	CK834036	CK834036	4058164 B
457	118.2	3.8	779	7	CF288502	CF288502	AGENCOURT
458	118	3.8	373	5	BY017370	BY017370	BY017370
c 459	118	3.8	428	6	CB059945	CB059945	4010160 B
460	118	3.8	763	5	BU612234	BU612234	UI-M-EW0-
461	117.8	3.7	409	5	BY506868	BY506868	BY506868
462	117.6	3.7	325	2	BB138812	BB138812	BB138812
463	117.6	3.7	329	2	BB560121	BB560121	BB560121
464	117.6	3.7	453	6	CB060019	CB060019	4010021 B

	465	117.6	3.7	654	5	BP754486	BP754486	BP754486
	466	117.4	3.7	504	1	AA110742	AA110742	mp55g10.r
	467	117.4	3.7	726	7	CK980025	CK980025	4111598 B
	468	117.2	3.7	336	2	BB165167	BB165167	BB165167
	469	117.2	3.7	407	5	BY516195	BY516195	BY516195
	470	117	3.7	149	6	CB062937	CB062937	4013191 B
	471	117	3.7	315	2	BB269712	BB269712	BB269712
	472	117	3.7	738	1	AL702888	AL702888	DKFZp686D
	473	117	3.7	917	5	BU916713	BU916713	AGENCOURT
	474	116.8	3.7	322	2	BB220489	BB220489	BB220489
	475	116.6	3.7	412	6	CB802007	CB802007	AMGNNUC:N
	476	116.6	3.7	426	2	AW767390	AW767390	da68e03.y
	477	116.6	3.7	711	7	CN401142	CN401142	170005328
	478	116.6	3.7	933	4	BG424061	BG424061	602448130
c	479	116.2	3.7	689	5	BX885697	BX885697	BX885697
	480	116	3.7	413	5	BY516984	BY516984	BY516984
	481	115.8	3.7	315	2	BB217943	BB217943	BB217943
	482	115.6	3.7	308	2	BB226784	BB226784	BB226784
	483	115.6	3.7	459	6	BY596859	BY596859	BY596859
	484	115.4	3.7	328	2	BB203677	BB203677	BB203677
	485	115	3.7	653	4	BG423200	BG423200	602450518
	486	115	3.7	1045	5	BX458922	BX458922	BX458922
	487	114.8	3.7	865	5	BQ962412	BQ962412	AGENCOURT
	488	114.6	3.6	413	6	BY577648	BY577648	BY577648
	489	114.4	3.6	318	2	BB221006	BB221006	BB221006
	490	114.4	3.6	3226	3	AK042751	AK042751	Mus muscu
	491	114.4	3.6	3329	3	AK082711	AK082711	Mus muscu
	492	114	3.6	268	2	BB594900	BB594900	BB594900
	493	113.8	3.6	552	7	CN664343	CN664343	A0811H09-
	494	113.4	3.6	408	5	BY159825	BY159825	BY159825
	495	113.4	3.6	1035	5	BQ944697	BQ944697	AGENCOURT
	496	113.2	3.6	262	2	BB733435	BB733435	BB733435
	497	113.2	3.6	297	2	BB082267	BB082267	BB082267
	498	113	3.6	294	2	BB369725	BB369725	BB369725
	499	113	3.6	311	2	BB319473	BB319473	BB319473
	500	113	3.6	647	4	BI159977	BI159977	602863854
	501	112.8	3.6	286	2	BB180038	BB180038	BB180038
	502	112.8	3.6	339	2	BB137126	BB137126	BB137126
	503	112.2	3.6	339	2	BB224502	BB224502	BB224502
	504	112.2	3.6	341	2	BB224286	BB224286	BB224286
	505	112.2	3.6	470	2	BB822561	BB822561	BB822561
	506	112	3.6	298	2	BB360425	BB360425	BB360425
	507	112	3.6	316	2	BB218778	BB218778	BB218778
	508	112	3.6	940	4	BG386070	BG386070	602455244
	509	111.8	3.6	287	2	BB179402	BB179402	BB179402
	510	111.8	3.6	395	5	BY019515	BY019515	BY019515
	511	111.8	3.6	691	4	BG422155	BG422155	602448882
	512	111.6	3.6	300	2	BB522135	BB522135	BB522135
	513	111.6	3.6	307	2	BB116702	BB116702	BB116702
	514	111.4	3.5	321	2	BB236584	BB236584	BB236584
	515	111.4	3.5	338	2	BB120467	BB120467	BB120467
	516	111.2	3.5	286	2	BB222636	BB222636	BB222636
	517	111.2	3.5	304	2	BB219012	BB219012	BB219012
	518	111.2	3.5	306	1	AV239830	AV239830	AV239830
	519	111.2	3.5	678	4	BM495316	BM495316	IpcGBr2_2
c	520	111.2	3.5	738	4	BM414643	BM414643	ECC00109
	521	111	3.5	277	2	BB324525	BB324525	BB324525

	522	110.8	3.5	295	2	BB511397	BB511397	BB511397
	523	110.6	3.5	1606	2	BF581604	BF581604	602099944
	524	110.4	3.5	788	4	BI161171	BI161171	602865624
	525	110.2	3.5	334	2	BB224542	BB224542	BB224542
	526	110	3.5	288	2	BB346214	BB346214	BB346214
	527	110	3.5	310	2	BB265127	BB265127	BB265127
c	528	110	3.5	344	1	AI070233	AI070233	UI-R-Y0-1
	529	109.8	3.5	306	2	BB530000	BB530000	BB530000
	530	109.8	3.5	487	7	CN367763	CN367763	170005322
	531	109.6	3.5	284	2	BB733429	BB733429	BB733429
	532	109.6	3.5	293	2	BB334189	BB334189	BB334189
	533	109.6	3.5	452	6	BY588670	BY588670	BY588670
	534	109.4	3.5	317	1	AV102365	AV102365	AV102365
	535	109.4	3.5	826	5	BU175920	BU175920	AGENCOURT
	536	109.4	3.5	1132	6	CD504092	CD504092	CDA66-A08
	537	109.2	3.5	357	5	BY193799	BY193799	BY193799
	538	109	3.5	110	6	CD631366	CD631366	56027747J
	539	109	3.5	292	2	BB440274	BB440274	BB440274
	540	109	3.5	295	2	BB179256	BB179256	BB179256
	541	109	3.5	298	2	BB257753	BB257753	BB257753
	542	108.8	3.5	309	2	BB124269	BB124269	BB124269
	543	108.8	3.5	310	2	BB335680	BB335680	BB335680
c	544	108.6	3.5	457	2	BE686664	BE686664	uw03e06.x
	545	108.4	3.4	292	2	BB173217	BB173217	BB173217
	546	108.4	3.4	299	2	BB276146	BB276146	BB276146
	547	108.2	3.4	168	2	AW345212	AW345212	25329 MAR
	548	108.2	3.4	311	2	BB143870	BB143870	BB143870
	549	108.2	3.4	910	4	BI161349	BI161349	602865754
	550	108	3.4	290	2	BB278479	BB278479	BB278479
	551	108	3.4	303	2	BB217218	BB217218	BB217218
	552	108	3.4	949	5	BU541977	BU541977	AGENCOURT
	553	108	3.4	3137	3	BC051979	BC051979	Mus muscu
	554	108	3.4	3907	3	AK031131	AK031131	Mus muscu
c	555	107.8	3.4	557	1	AU147993	AU147993	AU147993
	556	107.6	3.4	689	7	CO434547	CO434547	UI-M-HX0-
	557	107.6	3.4	1141	6	CA975355	CA975355	AGENCOURT
	558	107.4	3.4	289	2	BB007231	BB007231	BB007231
	559	107.4	3.4	305	2	BB500334	BB500334	BB500334
c	560	107.4	3.4	436	1	AA913136	AA913136	oi17h07.s
	561	107.4	3.4	569	7	CO258909	CO258909	4130136 B
c	562	107.4	3.4	734	5	BX674351	BX674351	BX674351
	563	107.2	3.4	312	2	BB445664	BB445664	BB445664
	564	107	3.4	284	2	BB507939	BB507939	BB507939
	565	106.8	3.4	289	2	BB496529	BB496529	BB496529
	566	106.8	3.4	290	2	BB368263	BB368263	BB368263
	567	106.8	3.4	292	2	BB354765	BB354765	BB354765
	568	106.8	3.4	304	2	BB336700	BB336700	BB336700
	569	106.8	3.4	328	2	BB220954	BB220954	BB220954
	570	106.6	3.4	686	4	BG469296	BG469296	602533135
	571	106.4	3.4	279	2	BB371226	BB371226	BB371226
	572	106.4	3.4	286	2	BB555504	BB555504	BB555504
	573	106.4	3.4	294	1	AV051876	AV051876	AV051876
	574	106.4	3.4	336	2	AW226731	AW226731	um60b09.y
c	575	106.4	3.4	488	4	BM151697	BM151697	TCBAP1E10
	576	106.2	3.4	281	2	BB346087	BB346087	BB346087
	577	106.2	3.4	725	7	CN429157	CN429157	170004252
	578	106	3.4	306	2	BB262651	BB262651	BB262651

579	106	3.4	318	2	BB243620	BB243620	BB243620
580	105.8	3.4	272	2	BB552255	BB552255	BB552255
581	105.8	3.4	283	2	BB128450	BB128450	BB128450
582	105.8	3.4	292	2	BB500569	BB500569	BB500569
583	105.8	3.4	976	5	BQ944147	BQ944147	AGENCOURT
584	105.6	3.4	281	2	BB348185	BB348185	BB348185
585	105.6	3.4	811	6	CD653578	CD653578	AGENCOURT
586	105.6	3.4	824	4	BM047429	BM047429	603628715
587	105.6	3.4	900	4	BG326356	BG326356	602425281
588	105.4	3.4	363	6	CD631362	CD631362	56027755J
c 589	105.4	3.4	603	7	CK849657	CK849657	972704 BA
c 590	105.4	3.4	742	5	BX910552	BX910552	BX910552
591	105.2	3.3	287	2	BB325091	BB325091	BB325091
592	105	3.3	394	6	CB776364	CB776364	AMGNNUC:N
593	105	3.3	860	5	BQ230111	BQ230111	AGENCOURT
594	105	3.3	924	4	BG326746	BG326746	602425623
595	105	3.3	963	5	BU552403	BU552403	AGENCOURT
596	105	3.3	1024	2	BE910319	BE910319	601503675
597	104.8	3.3	262	1	AV241169	AV241169	AV241169
598	104.8	3.3	306	2	BB500200	BB500200	BB500200
599	104.8	3.3	414	2	BB826095	BB826095	BB826095
600	104.8	3.3	795	6	CB245479	CB245479	UI-M-FY0-
601	104.8	3.3	911	5	BU501900	BU501900	AGENCOURT
602	104.8	3.3	919	5	BU173969	BU173969	AGENCOURT
603	104.6	3.3	282	2	BB532703	BB532703	BB532703
604	104.6	3.3	309	2	BB499049	BB499049	BB499049
605	104.2	3.3	310	2	BB236046	BB236046	BB236046
606	104.2	3.3	328	2	BB114323	BB114323	BB114323
607	104.2	3.3	414	6	BY578439	BY578439	BY578439
608	104.2	3.3	897	5	BQ219988	BQ219988	AGENCOURT
609	104.2	3.3	927	4	BG831583	BG831583	602765840
610	104	3.3	266	2	BB716868	BB716868	BB716868
611	104	3.3	283	2	BB528644	BB528644	BB528644
612	104	3.3	288	2	BB342818	BB342818	BB342818
613	104	3.3	2855	3	AK047067	AK047067	Mus muscu
614	103.8	3.3	298	2	BB283107	BB283107	BB283107
615	103.8	3.3	879	4	BG831929	BG831929	602765589
616	103.6	3.3	297	2	BB217129	BB217129	BB217129
617	103.6	3.3	307	2	BB500311	BB500311	BB500311
618	103.6	3.3	311	2	BB533042	BB533042	BB533042
619	103.6	3.3	315	2	BB122455	BB122455	BB122455
620	103.6	3.3	464	2	BB796655	BB796655	BB796655
621	103.4	3.3	314	2	BB239048	BB239048	BB239048
622	103.2	3.3	233	2	BB510804	BB510804	BB510804
623	103.2	3.3	286	2	BB178968	BB178968	BB178968
624	103.2	3.3	467	6	BY556536	BY556536	BY556536
625	103.2	3.3	583	4	BM488072	BM488072	pgm2n.pk0
626	103.2	3.3	868	1	AU140366	AU140366	AU140366
627	103	3.3	282	2	BB310767	BB310767	BB310767
628	103	3.3	619	1	AL118624	AL118624	DKFZp761F
629	102.8	3.3	269	2	BB313946	BB313946	BB313946
630	102.6	3.3	271	2	BB216188	BB216188	BB216188
631	102.6	3.3	579	5	BP375801	BP375801	BP375801
632	102.6	3.3	869	5	BM947242	BM947242	UI-M-EH0p
633	102.6	3.3	977	5	BU520216	BU520216	AGENCOURT
634	102.4	3.3	281	2	BB129002	BB129002	BB129002
635	102.2	3.3	268	2	BB216101	BB216101	BB216101

	636	102.2	3.3	271	2	BB555572	BB555572	BB555572
	637	102.2	3.3	285	2	BB324617	BB324617	BB324617
	638	102.2	3.3	342	2	BB223376	BB223376	BB223376
	639	102.2	3.3	644	1	AL803713	AL803713	AL803713
	640	102.2	3.3	659	7	CN695559	CN695559	E0366G09-
c	641	102	3.2	331	1	AI228417	AI228417	EST225112
	642	102	3.2	426	5	BY376368	BY376368	BY376368
c	643	102	3.2	654	6	CB420254	CB420254	593189 MA
	644	102	3.2	6875	3	BC032619	BC032619	Homo sapi
	645	101.8	3.2	222	2	BB150791	BB150791	BB150791
c	646	101.8	3.2	353	8	BZ845553	BZ845553	CH240_213
c	647	101.8	3.2	538	8	AQ434948	AQ434948	HS_5126_B
	648	101.8	3.2	779	5	BX396978	BX396978	BX396978
	649	101.8	3.2	1002	5	BQ068313	BQ068313	AGENCOURT
	650	101.6	3.2	315	2	BB116770	BB116770	BB116770
c	651	101.6	3.2	537	2	BE349814	BE349814	hq43e01.x
	652	101.2	3.2	317	2	BB213717	BB213717	BB213717
	653	101	3.2	254	2	BB172165	BB172165	BB172165
	654	101	3.2	2719	3	AK035993	AK035993	Mus muscu
	655	100.8	3.2	400	6	BY555199	BY555199	BY555199
c	656	100.8	3.2	492	1	AA023538	AA023538	mh75d07.r
	657	100.8	3.2	622	6	CD349441	CD349441	UI-M-FY0-
	658	100.6	3.2	505	4	BI898654	BI898654	479668 MA
	659	100.6	3.2	651	4	BM491746	BM491746	pqp2n.pk0
	660	100.4	3.2	285	2	BB177820	BB177820	BB177820
	661	100.2	3.2	699	4	BG830948	BG830948	602766844
	662	100.2	3.2	861	7	CO735048	CO735048	SlLE04c10
	663	100	3.2	224	2	BB499666	BB499666	BB499666
	664	100	3.2	286	2	BB110106	BB110106	BB110106
	665	100	3.2	316	2	BB145363	BB145363	BB145363
c	666	100	3.2	582	2	BF400607	BF400607	UI-R-CA0-
	667	100	3.2	786	7	CK365293	CK365293	AGENCOURT
	668	99.8	3.2	313	2	BB218103	BB218103	BB218103
	669	99.8	3.2	594	7	CN528682	CN528682	UI-M-HQ0-
	670	99.8	3.2	910	4	BG470201	BG470201	602533710
	671	99.8	3.2	3921	3	AK084922	AK084922	Mus muscu
	672	99.8	3.2	4374	3	AK031307	AK031307	Mus muscu
c	673	99.6	3.2	278	6	CD631370	CD631370	56027863J
c	674	99.6	3.2	703	1	AU170734	AU170734	AU170734
	675	99.6	3.2	844	7	CO735027	CO735027	SlLE04c10
	676	99.6	3.2	880	5	BU186709	BU186709	AGENCOURT
	677	99.4	3.2	286	2	BB333313	BB333313	BB333313
	678	99.4	3.2	772	4	BG829652	BG829652	602764012
	679	99.2	3.2	275	2	BB227524	BB227524	BB227524
	680	99.2	3.2	326	2	BB559836	BB559836	BB559836
	681	99	3.1	239	1	AV229642	AV229642	AV229642
	682	99	3.1	264	1	AV238667	AV238667	AV238667
	683	99	3.1	316	2	BB532106	BB532106	BB532106
c	684	99	3.1	319	4	BG377549	BG377549	UI-R-CU0-
	685	98.6	3.1	121	1	AI264258	AI264258	qk20b04.x
	686	98.6	3.1	278	2	BB176510	BB176510	BB176510
	687	98.6	3.1	317	1	AL655823	AL655823	AL655823
	688	98.4	3.1	100	4	BI002468	BI002468	MR3-HN015
	689	98.4	3.1	228	2	BB150964	BB150964	BB150964
	690	98.4	3.1	288	2	BB455324	BB455324	BB455324
	691	98.4	3.1	320	2	BB242404	BB242404	BB242404
	692	98.2	3.1	278	1	AV313234	AV313234	AV313234

693	98.2	3.1	308	2	BB263999	BB263999	BB263999
694	98.2	3.1	668	6	BY746861	BY746861	BY746861
695	98.2	3.1	4476	3	AK052232	AK052232	Mus muscu
696	98	3.1	235	2	BB716819	BB716819	BB716819
697	98	3.1	280	2	BB535881	BB535881	BB535881
698	97.6	3.1	203	4	BM105287	BM105287	508710 MA
699	97.6	3.1	369	5	BY020398	BY020398	BY020398
700	97.4	3.1	705	2	BE294211	BE294211	601172744
701	97.2	3.1	256	2	BB425457	BB425457	BB425457
702	97.2	3.1	281	1	AV235738	AV235738	AV235738
703	97.2	3.1	640	7	CN460578	CN460578	UI-M-HB0-
704	97.2	3.1	704	6	BY741417	BY741417	BY741417
705	96.8	3.1	223	1	AV229388	AV229388	AV229388
706	96.8	3.1	225	2	BB323996	BB323996	BB323996
707	96.8	3.1	236	2	BB019685	BB019685	BB019685
708	96.8	3.1	242	2	BB554948	BB554948	BB554948
709	96.8	3.1	273	2	BB010623	BB010623	BB010623
710	96.8	3.1	286	2	BB309932	BB309932	BB309932
711	96.8	3.1	496	7	CK390327	CK390327	K0817F12-
712	96.8	3.1	815	4	BG386811	BG386811	602455071
713	96.8	3.1	986	4	BG746534	BG746534	602703833
714	96.8	3.1	1394	5	BM926974	BM926974	AGENCOURT
715	96.6	3.1	234	2	BB357534	BB357534	BB357534
716	96.6	3.1	340	5	BY353322	BY353322	BY353322
717	96.6	3.1	342	2	BB241607	BB241607	BB241607
718	96.6	3.1	352	5	BY177856	BY177856	BY177856
719	96.6	3.1	396	5	BY201883	BY201883	BY201883
720	96.6	3.1	795	7	CO571948	CO571948	AGENCOURT
721	96.4	3.1	721	6	CA324424	CA324424	UI-M-FY0-
722	96.4	3.1	779	6	CA316005	CA316005	UI-M-FW0-
c 723	96.2	3.1	297	1	AI112352	AI112352	UI-R-Y0-m
c 724	96.2	3.1	297	1	AI576402	AI576402	UI-R-Y0-v
725	96.2	3.1	333	1	AV006222	AV006222	AV006222
726	96	3.1	400	5	BY158515	BY158515	BY158515
727	96	3.1	917	4	BG324311	BG324311	602423309
728	95.8	3.0	586	2	BF041445	BF041445	BP250015B
729	95.8	3.0	673	5	BM951984	BM951984	UI-M-EH0-
c 730	95.8	3.0	710	7	CK979615	CK979615	4111214 B
731	95.4	3.0	178	2	BF774071	BF774071	283623 MA
732	95.4	3.0	178	2	BF774072	BF774072	283624 MA
733	95.4	3.0	222	2	BB052672	BB052672	BB052672
734	95.4	3.0	238	2	BB034746	BB034746	BB034746
735	95.4	3.0	261	2	BB594935	BB594935	BB594935
736	95.4	3.0	278	2	BB173822	BB173822	BB173822
737	95.4	3.0	281	2	BB108075	BB108075	BB108075
738	95.4	3.0	436	5	BY487960	BY487960	BY487960
739	95.2	3.0	227	2	BB501238	BB501238	BB501238
740	95.2	3.0	243	1	AV232151	AV232151	AV232151
741	95.2	3.0	246	2	BB301620	BB301620	BB301620
742	95.2	3.0	297	2	BB135944	BB135944	BB135944
743	95.2	3.0	325	2	BB218380	BB218380	BB218380
c 744	95.2	3.0	434	4	BM193462	BM193462	TCBAP1Q13
745	95.2	3.0	490	1	AI365650	AI365650	ap20h08.x
746	95	3.0	380	5	BY165728	BY165728	BY165728
747	95	3.0	459	2	BB633829	BB633829	BB633829
748	95	3.0	519	2	BF046214	BF046214	BP250021A
749	95	3.0	541	2	BF045972	BF045972	BP250003B

	750	95	3.0	542	2	BF039059	BF039059	BP250018B
	751	95	3.0	648	6	CB419189	CB419189	592037 MA
	752	94.8	3.0	336	2	BB241589	BB241589	BB241589
	753	94.8	3.0	710	6	CA379066	CA379066	658061 NC
	754	94.8	3.0	4045	3	BC059007	BC059007	Mus muscu
	755	94.6	3.0	248	1	AV326941	AV326941	AV326941
	756	94.6	3.0	267	2	BB108706	BB108706	BB108706
	757	94.6	3.0	278	2	BB479760	BB479760	BB479760
	758	94.6	3.0	281	2	BB221528	BB221528	BB221528
	759	94.6	3.0	531	2	BE235013	BE235013	142239 MA
	760	94.6	3.0	703	5	BM951868	BM951868	UI-M-EH0-
	761	94.4	3.0	275	2	BB336194	BB336194	BB336194
	762	94.4	3.0	291	1	AV339535	AV339535	AV339535
	763	94.4	3.0	336	2	BB497526	BB497526	BB497526
	764	94.4	3.0	520	7	CN255484	CN255484	170005313
	765	94.4	3.0	954	4	BG829919	BG829919	602764325
	766	94.2	3.0	211	2	BB591302	BB591302	BB591302
	767	94.2	3.0	481	7	CK392759	CK392759	K0849F03-
	768	94.2	3.0	690	6	BY734086	BY734086	BY734086
	769	94.2	3.0	819	6	CD628635	CD628635	56097918H
c	770	94.2	3.0	828	5	BX665346	BX665346	BX665346
	771	94	3.0	230	2	BB254403	BB254403	BB254403
	772	94	3.0	301	2	BB335163	BB335163	BB335163
	773	94	3.0	589	4	BM150494	BM150494	TCBAP1D10
	774	93.8	3.0	227	2	BB213341	BB213341	BB213341
	775	93.8	3.0	249	2	BB324195	BB324195	BB324195
	776	93.8	3.0	575	2	BE245715	BE245715	TCBAP1D19
	777	93.6	3.0	225	2	BB270419	BB270419	BB270419
	778	93.6	3.0	229	2	BB217995	BB217995	BB217995
	779	93.6	3.0	237	2	BB431741	BB431741	BB431741
	780	93.6	3.0	238	2	BB356581	BB356581	BB356581
	781	93.6	3.0	239	1	AV238091	AV238091	AV238091
	782	93.6	3.0	241	1	AV341229	AV341229	AV341229
	783	93.6	3.0	241	2	BB073528	BB073528	BB073528
	784	93.6	3.0	254	2	BB258946	BB258946	BB258946
	785	93.6	3.0	259	2	BB215951	BB215951	BB215951
	786	93.6	3.0	478	2	BF654570	BF654570	278796 MA
	787	93.4	3.0	244	2	BB519336	BB519336	BB519336
	788	93.2	3.0	146	4	BI847990	BI847990	470271 MA
	789	93.2	3.0	244	2	BB242763	BB242763	BB242763
	790	93.2	3.0	265	1	AV286945	AV286945	AV286945
c	791	93.2	3.0	515	1	AL928354	AL928354	AL928354
	792	93.2	3.0	2340	9	AY421319	AY421319	Mus muscu
	793	93.2	3.0	3159	3	AK046502	AK046502	Mus muscu
	794	93.2	3.0	3225	9	AY400493	AY400493	Mus muscu
	795	93.2	3.0	3726	3	AK043386	AK043386	Mus muscu
	796	93	3.0	231	2	BB151727	BB151727	BB151727
	797	93	3.0	527	2	BF462568	BF462568	UI-M-CG0p
	798	93	3.0	725	6	CB520645	CB520645	UI-M-GI0-
	799	92.6	2.9	198	4	BI021066	BI021066	PM3-MT020
	800	92.6	2.9	228	2	BB073945	BB073945	BB073945
	801	92.6	2.9	289	2	BB720615	BB720615	BB720615
	802	92.6	2.9	377	5	BY165251	BY165251	BY165251
	803	92.6	2.9	546	6	CA406911	CA406911	1003060 H
	804	92.6	2.9	2575	3	AK031231	AK031231	Mus muscu
	805	92.4	2.9	274	2	BB177348	BB177348	BB177348
c	806	92.4	2.9	404	4	BM174889	BM174889	hippo_08_

807	92.2	2.9	587	5	BP214222	BP214222	BP214222
808	92.2	2.9	691	5	BM944530	BM944530	UI-M-EH0p
809	92	2.9	239	2	BB356352	BB356352	BB356352
810	92	2.9	274	2	BB551851	BB551851	BB551851
811	92	2.9	343	2	BB224139	BB224139	BB224139
812	92	2.9	492	7	CN333872	CN333872	170005325
813	92	2.9	518	2	BF714462	BF714462	mab01a06.
814	92	2.9	748	7	CN333873	CN333873	170006000
815	91.8	2.9	593	7	CN255490	CN255490	170006000
816	91.8	2.9	734	7	CO395136	CO395136	AGENCOURT
817	91.8	2.9	918	7	CF780707	CF780707	AGENCOURT
818	91.6	2.9	247	2	BB170802	BB170802	BB170802
c 819	91.6	2.9	434	1	AV608925	AV608925	AV608925
820	91.6	2.9	704	6	CB527136	CB527136	UI-M-FY0-
821	91.6	2.9	937	5	BU518484	BU518484	AGENCOURT
822	91.4	2.9	433	6	BY580507	BY580507	BY580507
823	91.4	2.9	600	5	BU925145	BU925145	7112-63 M
824	91.2	2.9	281	6	CD631369	CD631369	56027863H
825	91.2	2.9	543	6	CD216128	CD216128	pgp2n.pk0
826	91.2	2.9	756	4	BI645497	BI645497	603275463
827	91	2.9	229	1	AV232333	AV232333	AV232333
828	91	2.9	625	6	CB247662	CB247662	UI-M-FI0-
829	91	2.9	740	7	CF532104	CF532104	UI-M-FY0-
c 830	90.8	2.9	228	6	CB168395	CB168395	HSF603268
831	90.8	2.9	657	7	CN788571	CN788571	4122921 B
832	90.6	2.9	283	1	AV224722	AV224722	AV224722
833	90.6	2.9	827	4	BF981141	BF981141	602310407
834	90.4	2.9	230	2	BB270171	BB270171	BB270171
835	90.4	2.9	239	2	BB267673	BB267673	BB267673
836	90.4	2.9	369	5	BY170960	BY170960	BY170960
837	90.2	2.9	238	2	BB356191	BB356191	BB356191
838	89.8	2.9	235	2	BB170781	BB170781	BB170781
839	89.8	2.9	245	2	BB149370	BB149370	BB149370
840	89.8	2.9	896	4	BI457032	BI457032	603185949
841	89.6	2.9	279	2	BB177200	BB177200	BB177200
842	89.4	2.8	256	7	CN223998	CN223998	WLA052F08
843	89.4	2.8	574	5	BM946983	BM946983	UI-M-EH0p
844	89.2	2.8	329	2	BB499916	BB499916	BB499916
845	89	2.8	231	2	BB148551	BB148551	BB148551
846	89	2.8	255	2	BB001987	BB001987	BB001987
847	89	2.8	456	5	BY491040	BY491040	BY491040
848	89	2.8	509	2	AW964929	AW964929	EST376897
849	88.8	2.8	228	2	BB341090	BB341090	BB341090
850	88.8	2.8	232	2	BB009287	BB009287	BB009287
851	88.6	2.8	593	5	BP249762	BP249762	BP249762
c 852	88.6	2.8	873	5	BX770216	BX770216	BX770216
853	88.2	2.8	567	4	BG710581	BG710581	pg11n.pk0
854	88	2.8	282	2	BB531669	BB531669	BB531669
855	88	2.8	745	6	CA388534	CA388534	670926 NC
856	87.8	2.8	256	5	BM948107	BM948107	UI-M-EG0p
857	87.8	2.8	824	4	BI161136	BI161136	602865179
858	87.4	2.8	229	2	BB173708	BB173708	BB173708
859	87.4	2.8	234	2	BB717863	BB717863	BB717863
860	87.4	2.8	340	5	BY207534	BY207534	BY207534
861	87.4	2.8	745	5	BU055918	BU055918	UI-M-FO0-
862	87.2	2.8	229	2	BB239543	BB239543	BB239543
863	87.2	2.8	240	2	BB326658	BB326658	BB326658

	864	87	2.8	697	2	AW134401	AW134401	fi18h09.y
	865	87	2.8	770	6	CD628629	CD628629	56097478H
	866	86.8	2.8	242	2	BB359459	BB359459	BB359459
	867	86.8	2.8	258	1	AV375018	AV375018	AV375018
	868	86.6	2.8	433	5	BY376940	BY376940	BY376940
	869	86.6	2.8	917	2	BE908445	BE908445	601503077
	870	86.6	2.8	923	4	BI665624	BI665624	603289613
	871	86.6	2.8	2376	3	AK045236	AK045236	Mus muscu
	872	86.4	2.7	216	2	BB323957	BB323957	BB323957
	873	86.4	2.7	462	6	CD553207	CD553207	B0356E10-
	874	86.4	2.7	621	4	BM738310	BM738310	K-EST0003
	875	86.4	2.7	631	6	BY724321	BY724321	BY724321
	876	86.4	2.7	632	2	BE270240	BE270240	601186027
c	877	86.4	2.7	646	2	BF322402	BF322402	maa24f04.
	878	86.4	2.7	966	5	BQ715428	BQ715428	AGENCOURT
	879	86.2	2.7	208	2	BB079119	BB079119	BB079119
	880	86.2	2.7	242	1	AV381879	AV381879	AV381879
	881	86.2	2.7	249	2	BB215799	BB215799	BB215799
	882	86.2	2.7	929	5	BQ917819	BQ917819	AGENCOURT
	883	86	2.7	211	2	BB184958	BB184958	BB184958
	884	86	2.7	280	2	BB142942	BB142942	BB142942
	885	86	2.7	570	2	BE407695	BE407695	601299714
	886	85.8	2.7	543	2	AW966670	AW966670	EST378744
	887	85.8	2.7	757	4	BI735927	BI735927	603360340
	888	85.6	2.7	224	2	BB171694	BB171694	BB171694
	889	85.6	2.7	245	1	AV232593	AV232593	AV232593
	890	85.6	2.7	673	7	CN401143	CN401143	170005322
	891	85.6	2.7	900	6	CA321459	CA321459	UI-M-FW0-
	892	85.6	2.7	965	5	BU845252	BU845252	AGENCOURT
	893	85.6	2.7	977	5	BU855862	BU855862	AGENCOURT
	894	85.4	2.7	284	2	BB181557	BB181557	BB181557
	895	85.4	2.7	356	5	BY204763	BY204763	BY204763
	896	85.4	2.7	515	2	BB633428	BB633428	BB633428
	897	85.2	2.7	207	2	BB214019	BB214019	BB214019
	898	85.2	2.7	620	5	BM943707	BM943707	UI-M-EH0p
	899	85	2.7	306	2	BB030476	BB030476	BB030476
	900	84.6	2.7	232	2	BB262137	BB262137	BB262137
	901	84.6	2.7	264	2	BB534094	BB534094	BB534094
	902	84.6	2.7	266	2	BB196113	BB196113	BB196113
	903	84.6	2.7	698	5	BU227771	BU227771	603800481
	904	84.4	2.7	628	6	CA318117	CA318117	UI-M-FW0-
	905	84.4	2.7	1010	5	BX360753	BX360753	BX360753
	906	84.4	2.7	1246	2	BF166143	BF166143	601776590
	907	84.2	2.7	218	2	BB213301	BB213301	BB213301
	908	84	2.7	456	5	BY155480	BY155480	BY155480
	909	84	2.7	790	6	CB248961	CB248961	UI-M-EX0-
	910	84	2.7	864	5	BU156223	BU156223	AGENCOURT
	911	83.8	2.7	214	2	BB588963	BB588963	BB588963
	912	83.6	2.7	249	1	AV381817	AV381817	AV381817
	913	83.4	2.7	270	2	BB177951	BB177951	BB177951
	914	83.4	2.7	720	6	CD628637	CD628637	56098002H
	915	83.4	2.7	777	6	CB248692	CB248692	UI-M-EX0-
	916	83	2.6	227	2	BB216867	BB216867	BB216867
c	917	83	2.6	338	6	CB060198	CB060198	4010590 B
	918	83	2.6	691	5	BQ180084	BQ180084	UI-M-EW0-
	919	82.8	2.6	334	5	BY023564	BY023564	BY023564
	920	82.8	2.6	425	1	AV665430	AV665430	AV665430

	921	82.8	2.6	511	6	CA383610	CA383610	663812	NC
	922	82.8	2.6	647	5	BM950623	BM950623	UI-M-EH0p	
	923	82.6	2.6	410	5	BU428839	BU428839	UI-HF-BN0	
	924	82.6	2.6	445	2	BE244550	BE244550	TCBAP1D11	
	925	82.6	2.6	492	2	BE018639	BE018639	bb83a12.y	
	926	82.6	2.6	549	2	AW655369	AW655369	106098	MA
	927	82.6	2.6	638	2	AW245910	AW245910	2822888.5	
c	928	82.4	2.6	139	7	CK942460	CK942460	4066200	B
	929	82.4	2.6	227	2	BB221591	BB221591	BB221591	
	930	82.4	2.6	569	2	AW499893	AW499893	UI-HF-BN0	
	931	82.4	2.6	582	5	BP348794	BP348794	BP348794	
	932	82	2.6	200	6	BY589580	BY589580	BY589580	
	933	82	2.6	224	2	BB170950	BB170950	BB170950	
	934	82	2.6	314	5	BY347200	BY347200	BY347200	
	935	82	2.6	855	5	BQ770087	BQ770087	UI-M-FI0-	
	936	81.8	2.6	228	1	AV231620	AV231620	AV231620	
c	937	81.6	2.6	377	2	BE246473	BE246473	TCBAP1E47	
	938	81.4	2.6	2292	9	AY402638	AY402638	Mus muscu	
	939	81.2	2.6	707	6	BY733150	BY733150	BY733150	
	940	81.2	2.6	821	7	CK846765	CK846765	969310	MA
	941	81	2.6	553	7	CN684594	CN684594	E0195H06-	
	942	80.8	2.6	378	2	BB745658	BB745658	BB745658	
	943	80.8	2.6	459	4	BJ043336	BJ043336	BJ043336	
	944	80.8	2.6	479	2	BF731124	BF731124	mab81e06.	
	945	80.4	2.6	240	2	BB301102	BB301102	BB301102	
	946	80.4	2.6	405	6	CB808856	CB808856	AMGNNUC:S	
	947	80.4	2.6	625	6	CD348364	CD348364	UI-M-FY0-	
c	948	80.4	2.6	763	6	CD619057	CD619057	56030577H	
	949	80.4	2.6	785	4	BI194687	BI194687	602946246	
	950	80.4	2.6	797	7	CO404183	CO404183	AGENCOURT	
	951	80.4	2.6	890	5	BU856543	BU856543	AGENCOURT	
	952	80.2	2.6	363	5	BY344602	BY344602	BY344602	
	953	80.2	2.6	850	5	BM944264	BM944264	UI-M-EH0p	
	954	80.2	2.6	900	7	CK799299	CK799299	AGENCOURT	
c	955	79.8	2.5	307	4	BF961259	BF961259	PM1-NN120	
	956	79.8	2.5	700	6	CD628633	CD628633	56097902H	
	957	79.6	2.5	233	2	BB134411	BB134411	BB134411	
	958	79.6	2.5	237	2	BB593564	BB593564	BB593564	
	959	79.6	2.5	268	2	BB383954	BB383954	BB383954	
c	960	79.6	2.5	426	4	BF954455	BF954455	MR4-NN020	
	961	79.6	2.5	718	4	BG475468	BG475468	602491461	
	962	79.6	2.5	801	5	BX313585	BX313585	BX313585	
	963	79.6	2.5	922	5	BQ943695	BQ943695	AGENCOURT	
	964	79.6	2.5	2349	9	AY421317	AY421317	Homo sapi	
	965	79.4	2.5	581	5	BX310430	BX310430	BX310430	
	966	79.4	2.5	643	5	BX087763	BX087763	BX087763	
	967	79.2	2.5	362	5	BY344235	BY344235	BY344235	
c	968	79.2	2.5	457	2	AW462107	AW462107	BP230008A	
	969	79.2	2.5	647	2	BE907509	BE907509	601497468	
	970	79	2.5	295	2	BB354856	BB354856	BB354856	
	971	79	2.5	453	2	AW500044	AW500044	UI-HF-BN0	
	972	79	2.5	593	5	BQ266902	BQ266902	NISC_ff15	
	973	79	2.5	978	5	BQ963608	BQ963608	AGENCOURT	
	974	78.8	2.5	696	7	CK974651	CK974651	4105581	B
	975	78.8	2.5	826	6	CD628641	CD628641	56097486H	
	976	78.6	2.5	474	2	AW659439	AW659439	96609	MAR
c	977	78.6	2.5	599	2	BF357811	BF357811	RC2-LT000	

978	78.4	2.5	450	2	BE653346	BE653346	UI-M-AL1-
979	78.4	2.5	490	6	CA531840	CA531840	C0325D06-
980	78.4	2.5	645	7	CF170234	CF170234	B0824E08-
981	78.4	2.5	696	7	CF168782	CF168782	B0804F02-
982	78.4	2.5	719	7	CK636248	CK636248	UI-M-HN0-
983	78.2	2.5	225	2	BB443283	BB443283	BB443283
984	78.2	2.5	231	2	BB148230	BB148230	BB148230
c 985	78.2	2.5	254	6	CB469624	CB469624	sn09_H09.
986	78	2.5	239	2	BB109818	BB109818	BB109818
987	77.8	2.5	219	1	AV369146	AV369146	AV369146
c 988	77.8	2.5	551	2	BF516420	BF516420	UI-H-BW1-
989	77.6	2.5	175	1	AV375624	AV375624	AV375624
990	77.2	2.5	887	5	BU906435	BU906435	AGENCOURT
c 991	77	2.4	703	5	BM936326	BM936326	UI-M-CG0p
992	76.8	2.4	438	7	CF535009	CF535009	UI-M-GH0-
993	76.8	2.4	687	4	BG327618	BG327618	602426612
994	76.6	2.4	357	1	AI877089	AI877089	vz73g04.r
995	76.6	2.4	443	4	BM484413	BM484413	538266 MA
996	76.6	2.4	469	7	CN429211	CN429211	170005327
997	76.6	2.4	862	1	AU118557	AU118557	AU118557
c 998	76.4	2.4	106	6	CD631365	CD631365	56027747H
999	76.2	2.4	234	1	AV250428	AV250428	AV250428
1000	76.2	2.4	904	5	BU145486	BU145486	AGENCOURT
1001	76.2	2.4	2224	9	AY421318	AY421318	Pan trogl
1002	76	2.4	77	6	CD631368	CD631368	56027839J
1003	76	2.4	223	2	BB330942	BB330942	BB330942
1004	76	2.4	283	6	CD631364	CD631364	56027739J
1005	76	2.4	600	4	BI986000	BI986000	3154-38 M
1006	75.8	2.4	225	2	BB214723	BB214723	BB214723
1007	75.8	2.4	699	6	CD628631	CD628631	56097494H
1008	75.2	2.4	234	2	BB327897	BB327897	BB327897
1009	75.2	2.4	464	2	BE263633	BE263633	601192057
1010	75.2	2.4	658	4	BG424478	BG424478	602447602
1011	75.2	2.4	715	5	BX849809	BX849809	BX849809
1012	75.2	2.4	865	5	BX844237	BX844237	BX844237
1013	75.2	2.4	917	5	BQ224963	BQ224963	AGENCOURT
1014	75	2.4	158	2	BB244145	BB244145	BB244145
1015	75	2.4	622	6	CA324358	CA324358	UI-M-FY0-
1016	75	2.4	1129	5	BQ071719	BQ071719	AGENCOURT
c1017	74.8	2.4	462	4	BF944916	BF944916	CM1-NN019
c1018	74.6	2.4	130	2	BE349795	BE349795	hq43b12.x
1019	74.6	2.4	789	4	BI686539	BI686539	603313631
c1020	74.4	2.4	228	1	AI323583	AI323583	mp57e06.x
1021	74.4	2.4	467	2	BF443467	BF443467	260957 MA
1022	74.4	2.4	661	7	CN333878	CN333878	170005315
1023	74.4	2.4	748	7	CF747865	CF747865	UI-M-HE0-
1024	74.4	2.4	763	7	CN461035	CN461035	UI-M-HB0-
1025	74	2.4	410	2	AW477508	AW477508	12794 MAR
1026	74	2.4	725	7	CN429210	CN429210	170004241
1027	74	2.4	771	7	CF285178	CF285178	AGENCOURT
1028	73.8	2.3	182	2	BB083305	BB083305	BB083305
1029	73.8	2.3	228	1	AV173854	AV173854	AV173854
1030	73.8	2.3	989	6	CA454865	CA454865	AGENCOURT
1031	73.6	2.3	414	6	CB801298	CB801298	AMGNNUC:M
1032	73.4	2.3	184	2	BB216676	BB216676	BB216676
1033	73.4	2.3	878	4	BM042998	BM042998	603619122
1034	73.4	2.3	1019	1	AL541401	AL541401	AL541401

1035	73.2	2.3	154	1	AV230195	AV230195	AV230195
1036	73.2	2.3	430	6	CB760771	CB760771	AMGNNUC:T
1037	73.2	2.3	580	7	CN333883	CN333883	170005318
1038	73	2.3	275	2	BB604391	BB604391	BB604391
c1039	73	2.3	526	5	BX267431	BX267431	BX267431
c1040	73	2.3	526	5	BX270851	BX270851	BX270851
c1041	73	2.3	528	5	BX270850	BX270850	BX270850
1042	73	2.3	716	7	CF747885	CF747885	UI-M-HE0-
1043	73	2.3	851	6	CD653925	CD653925	AGENCOURT
c1044	73	2.3	963	9	CC841964	CC841964	NDL.130G1
1045	73	2.3	3225	9	AY400492	AY400492	Pan trogl
c1046	72.8	2.3	355	6	CD631361	CD631361	56027755H
1047	72.8	2.3	569	6	CA352454	CA352454	623718 NC
1048	72.6	2.3	636	5	BQ109297	BQ109297	imageqc_6
c1049	72.6	2.3	820	1	AI800602	AI800602	wg12d10.x
1050	72.2	2.3	488	5	BQ044885	BQ044885	UI-M-EH0p
1051	72.2	2.3	539	7	CO051028	CO051028	Le_mx0_22
1052	72.2	2.3	843	7	CF995086	CF995086	AGENCOURT
1053	72.2	2.3	914	6	CA792253	CA792253	AGENCOURT
1054	71.8	2.3	228	2	BB213582	BB213582	BB213582
1055	71.4	2.3	680	6	BY735266	BY735266	BY735266
1056	71.4	2.3	715	6	CD628625	CD628625	56097386H
1057	71.4	2.3	3225	9	AY400491	AY400491	Homo sapi
1058	71.2	2.3	381	6	CB809999	CB809999	AMGNNUC:N
c1059	71.2	2.3	396	2	BE245837	BE245837	TCBAP1E19
1060	71.2	2.3	436	6	BY536630	BY536630	BY536630
1061	71.2	2.3	1005	5	BU553834	BU553834	AGENCOURT
1062	70.8	2.3	169	7	CK377833	CK377833	lai09b12.
1063	70.8	2.3	188	1	AV230685	AV230685	AV230685
1064	70.8	2.3	277	2	BB529518	BB529518	BB529518
1065	70.8	2.3	805	6	CD656935	CD656935	AGENCOURT
1066	70.6	2.2	767	9	CL640550	CL640550	G076F10 G
c1067	70.2	2.2	151	6	CB475278	CB475278	jns105_D0
1068	70.2	2.2	390	9	CL640447	CL640447	G074G07 G
c1069	70	2.2	228	1	AI837906	AI837906	UI-M-AL0-
1070	70	2.2	604	2	BE283742	BE283742	601103987
1071	70	2.2	777	7	CK479930	CK479930	AGENCOURT
1072	70	2.2	1911	9	AY403380	AY403380	Homo sapi
1073	69.8	2.2	163	7	CF424452	CF424452	lad30g10.
c1074	69.8	2.2	285	2	BF874390	BF874390	QV2-ET010
1075	69.6	2.2	157	2	BB151796	BB151796	BB151796
1076	69.6	2.2	266	7	Z28925	Z28925	HSBC1H081 S
1077	69.6	2.2	765	4	BI823626	BI823626	603038515
1078	69.6	2.2	832	7	CN534073	CN534073	UI-M-HO0-
1079	69.6	2.2	1154	4	BM462308	BM462308	AGENCOURT
1080	69.4	2.2	701	4	BI194321	BI194321	602947742
1081	69.2	2.2	343	5	BY173287	BY173287	BY173287
1082	69.2	2.2	555	1	AI641288	AI641288	fc13a11.y
1083	69	2.2	866	4	BG923853	BG923853	602824656
1084	69	2.2	894	4	BG422248	BG422248	602446883
1085	68.8	2.2	638	6	CD215884	CD215884	pgp2n.pk0
1086	68.8	2.2	641	7	CN665211	CN665211	A0823B11-
1087	68.8	2.2	728	6	CD628623	CD628623	56097378H
1088	68.6	2.2	695	5	BQ769222	BQ769222	UI-M-FC0-
c1089	68.4	2.2	325	2	BE246184	BE246184	TCBAP2E06
1090	68.4	2.2	518	6	BY593368	BY593368	BY593368
1091	68.2	2.2	439	1	AA263826	AA263826	LD07023.5

1092	68	2.2	786	1	AL584324	AL584324	AL584324
1093	67.8	2.2	243	7	CO187281	CO187281	EK027722.
1094	67.8	2.2	591	1	AL711630	AL711630	DKFZp686N
1095	67.8	2.2	626	7	CF535272	CF535272	UI-M-GH0-
1096	67.8	2.2	689	7	CN460658	CN460658	UI-M-HB0-
1097	67.8	2.2	849	7	CF726328	CF726328	UI-M-HB0-
1098	67.6	2.2	177	2	BB262424	BB262424	BB262424
1099	67.6	2.2	200	2	BB213365	BB213365	BB213365
1100	67.6	2.2	562	4	BM090629	BM090629	igl6e01.y
1101	67.6	2.2	582	5	BP215174	BP215174	BP215174
1102	67.6	2.2	768	6	CD619058	CD619058	56030577J
1103	67.6	2.2	4847	3	BC083186	BC083186	Mus muscu
1104	67.2	2.1	238	2	BB593587	BB593587	BB593587
1105	67.2	2.1	394	6	CB547006	CB547006	AMGNNUC:S
1106	67.2	2.1	692	7	CN236752	CN236752	RJB124H02
1107	67.2	2.1	3394	3	AK053632	AK053632	Mus muscu
1108	67	2.1	170	2	BB218573	BB218573	BB218573
1109	66.8	2.1	639	7	CV022901	CV022901	340 Full
c1110	66.8	2.1	710	1	AI638881	AI638881	tt08d08.x
1111	66.8	2.1	967	5	BX460723	BX460723	BX460723
1112	66.6	2.1	185	2	BB008412	BB008412	BB008412
1113	66.6	2.1	291	6	CB710224	CB710224	AMGNNUC:N
1114	66.6	2.1	813	6	CA320357	CA320357	UI-M-FW0-
1115	66.4	2.1	656	7	CF728356	CF728356	UI-M-HB0-
1116	66.4	2.1	777	7	CF742166	CF742166	UI-M-HB0-
1117	66.4	2.1	813	2	BE872958	BE872958	601451552
c1118	66.2	2.1	197	2	AW048928	AW048928	UI-M-BH1-
1119	66	2.1	639	6	CD502318	CD502318	CDA56-A04
1120	66	2.1	801	7	CK679212	CK679212	ZF101-P00
1121	65.6	2.1	668	7	CK836913	CK836913	4062174 B
1122	65.6	2.1	690	4	BG333712	BG333712	602460715
1123	65.4	2.1	264	2	BB532400	BB532400	BB532400
1124	65.4	2.1	580	5	BP326398	BP326398	BP326398
1125	65.2	2.1	343	5	BY351503	BY351503	BY351503
1126	65.2	2.1	731	7	CN458596	CN458596	UI-M-HB0-
1127	65.2	2.1	834	7	CF740100	CF740100	UI-M-HD0-
1128	65.2	2.1	1372	3	AK039355	AK039355	Mus muscu
1129	65	2.1	497	6	CA319520	CA319520	UI-M-FW0-
1130	65	2.1	701	6	BY736064	BY736064	BY736064
1131	64.8	2.1	278	2	BB523398	BB523398	BB523398
1132	64.8	2.1	597	7	CN255479	CN255479	170005322
1133	64.8	2.1	771	7	CK791448	CK791448	AGENCOURT
1134	64.6	2.1	320	5	BY346988	BY346988	BY346988
1135	64.2	2.0	346	5	BY018991	BY018991	BY018991
1136	64	2.0	147	1	AV315332	AV315332	AV315332
1137	64	2.0	576	7	CN333867	CN333867	170005318
1138	64	2.0	725	7	CN457302	CN457302	UI-M-HN0-
1139	64	2.0	757	7	CK635851	CK635851	UI-M-HN0-
1140	64	2.0	942	1	AU078986	AU078986	AU078986
1141	64	2.0	976	9	CNS02YCR	AL219492	Tetraodon
1142	64	2.0	1155	2	BF531775	BF531775	602072681
1143	63.8	2.0	591	4	BJ074142	BJ074142	BJ074142
1144	63.8	2.0	655	4	BJ063284	BJ063284	BJ063284
1145	63.8	2.0	723	4	BI870437	BI870437	603395690
1146	63.8	2.0	900	6	C82295	C82295	C82295 Leuk
1147	63.8	2.0	2319	9	AY402636	AY402636	Homo sapi
1148	63.8	2.0	2960	3	AK043634	AK043634	Mus muscu

1149	63.8	2.0	3154	3	AK033597	AK033597	Mus muscu
1150	63.8	2.0	3287	3	AK048364	AK048364	Mus muscu
1151	63.8	2.0	3292	3	AK037034	AK037034	Mus muscu
1152	63.8	2.0	3436	3	AK014333	AK014333	Mus muscu
1153	63.6	2.0	233	2	BB327844	BB327844	BB327844
1154	63.6	2.0	573	6	CD214656	CD214656	pgm2n.pk0
1155	63.6	2.0	831	7	CO433634	CO433634	UI-M-HX0-
1156	63.4	2.0	571	7	CN401141	CN401141	170006000
1157	63.4	2.0	676	6	CD803405	CD803405	UI-M-GV0-
1158	63.4	2.0	889	1	AU050267	AU050267	AU050267
1159	63.2	2.0	700	4	BI143486	BI143486	602907665
1160	63	2.0	232	2	BB169302	BB169302	BB169302
1161	63	2.0	370	5	BY028015	BY028015	BY028015
1162	62.8	2.0	1020	6	CB590629	CB590629	AGENCOURT
1163	62.6	2.0	214	2	BB269367	BB269367	BB269367
c1164	62.6	2.0	384	2	AW900477	AW900477	CM0-NN100
1165	62.6	2.0	469	7	CN429155	CN429155	170005318
1166	62.6	2.0	508	6	CD675182	CD675182	fs20a08.y
1167	62.6	2.0	602	5	BQ749127	BQ749127	UI-M-FD0-
1168	62.6	2.0	939	5	BU915658	BU915658	AGENCOURT
1169	62.4	2.0	150	1	AV237564	AV237564	AV237564
1170	62.4	2.0	555	7	CN670016	CN670016	A0887D08-
1171	62.4	2.0	2289	9	AY402637	AY402637	Pan trogl
1172	62.2	2.0	178	2	BB603730	BB603730	BB603730
1173	62.2	2.0	857	4	BI161471	BI161471	602865054
1174	62	2.0	857	2	BF580228	BF580228	602099043
1175	62	2.0	883	5	BU224821	BU224821	603948128
1176	61.8	2.0	469	1	AU279333	AU279333	AU279333
1177	61.8	2.0	685	1	AL637843	AL637843	AL637843
1178	61.8	2.0	856	7	CO246694	CO246694	AGENCOURT
1179	61.6	2.0	212	2	BB587253	BB587253	BB587253
c1180	61.6	2.0	580	7	CO302404	CO302404	EK184063.
1181	61.6	2.0	859	5	BQ571689	BQ571689	UI-M-FC0-
1182	61.4	2.0	155	2	BB222407	BB222407	BB222407
c1183	61.4	2.0	1056	9	CNS00JQN	AL076816	Drosophil
1184	61.2	1.9	170	2	BB113286	BB113286	BB113286
1185	61.2	1.9	490	7	CN538039	CN538039	UI-M-HS0-
1186	61.2	1.9	1084	4	BG479750	BG479750	602526948
1187	61	1.9	203	1	AA326134	AA326134	EST29247
c1188	61	1.9	398	1	AI787249	AI787249	uj58a10.x
1189	61	1.9	421	7	CN401145	CN401145	170004241
1190	60.8	1.9	441	6	CA871124	CA871124	K0908A03-
1191	60.8	1.9	1039	5	BX458912	BX458912	BX458912
1192	60.8	1.9	1170	2	BF345508	BF345508	602019266
1193	60.6	1.9	207	7	CN700205	CN700205	E0431G12-
1194	60.6	1.9	675	6	BY718955	BY718955	BY718955
1195	60.6	1.9	959	1	AL551337	AL551337	AL551337
c1196	60	1.9	395	4	BF947978	BF947978	CM1-NN019
c1197	60	1.9	587	6	CB585337	CB585337	AMGNNUC:U
1198	59.8	1.9	812	6	CA317902	CA317902	UI-M-FW0-
1199	59.6	1.9	403	7	CF535184	CF535184	UI-M-GI0-
1200	59.6	1.9	765	7	CK366996	CK366996	AGENCOURT
1201	59.4	1.9	546	2	BF194361	BF194361	246370 MA
1202	59.4	1.9	736	5	BM947302	BM947302	UI-M-EH0p
1203	59.2	1.9	986	4	BI686422	BI686422	603315567
1204	59	1.9	265	7	M78717	M78717	EST00865 Hi
c1205	59	1.9	373	4	BG998374	BG998374	PM4-HT130

1206	59	1.9	983	5	BQ879085	BQ879085	AGENCOURT
1207	59	1.9	2227	9	AY403445	AY403445	Mus muscu
1208	58.8	1.9	342	2	BE246502	BE246502	TCBAP1D47
c1209	58.8	1.9	595	5	BX672477	BX672477	BX672477
c1210	58.8	1.9	718	7	CK776486	CK776486	967641 MA
1211	58.8	1.9	814	2	BF348116	BF348116	602022006
1212	58.8	1.9	944	5	BQ931286	BQ931286	AGENCOURT
1213	58.6	1.9	338	2	BE246248	BE246248	TCBAP2D06
1214	58.6	1.9	456	4	BG015017	BG015017	PM1-GN018
1215	58.6	1.9	498	1	AA190645	AA190645	zq44a06.r
1216	58.6	1.9	628	6	CB577722	CB577722	AMGNNUC:N
1217	58.6	1.9	987	2	BE727277	BE727277	601560955
1218	58.4	1.9	581	5	BP198298	BP198298	BP198298
1219	58.4	1.9	595	1	AL678465	AL678465	AL678465
1220	58.4	1.9	599	1	AL678560	AL678560	AL678560
1221	58.4	1.9	766	4	BI335382	BI335382	602997946
1222	58.4	1.9	1109	4	BM547638	BM547638	AGENCOURT
1223	58.4	1.9	1121	4	BM477901	BM477901	AGENCOURT
1224	58.2	1.9	480	5	BY247585	BY247585	BY247585
1225	58.2	1.9	581	5	BP196129	BP196129	BP196129
1226	58.2	1.9	608	1	AI258757	AI258757	LP02029.5
1227	58.2	1.9	674	1	AU138132	AU138132	AU138132
1228	58.2	1.9	921	2	BF237200	BF237200	602028155
1229	57.8	1.8	148	1	AV378912	AV378912	AV378912
1230	57.8	1.8	173	2	AW983563	AW983563	RC3-HN000
1231	57.8	1.8	419	6	CB764881	CB764881	AMGNNUC:N
1232	57.8	1.8	634	6	CB548205	CB548205	AMGNNUC:C
1233	57.8	1.8	634	6	CB577061	CB577061	AMGNNUC:C
1234	57.8	1.8	840	6	CB990331	CB990331	AGENCOURT
1235	57.6	1.8	253	6	CA394719	CA394719	cs55b06.y
1236	57.6	1.8	554	4	BI683327	BI683327	464671 MA
1237	57.6	1.8	574	4	BJ068614	BJ068614	BJ068614
1238	57.6	1.8	631	6	CA876860	CA876860	K0951D08-
1239	57.6	1.8	703	4	BJ733929	BJ733929	BJ733929
1240	57.6	1.8	767	7	CO246012	CO246012	AGENCOURT
1241	57.6	1.8	911	5	BQ278955	BQ278955	AGENCOURT
1242	57.4	1.8	463	4	BI515157	BI515157	BB160017B
1243	57.4	1.8	611	5	BX852769	BX852769	BX852769
1244	57.4	1.8	755	4	BG326539	BG326539	602425385
1245	57.4	1.8	770	6	CA945576	CA945576	UI-M-FD0-
c1246	57.2	1.8	573	2	BE070335	BE070335	QV4-BT040
1247	57.2	1.8	690	1	AU134748	AU134748	AU134748
1248	57.2	1.8	698	5	BX344176	BX344176	BX344176
1249	57.2	1.8	811	7	CK482600	CK482600	AGENCOURT
1250	57.2	1.8	990	4	BI652258	BI652258	603299702
1251	57.2	1.8	1018	4	BI519944	BI519944	603071726
1252	57	1.8	444	6	BY531725	BY531725	BY531725
1253	57	1.8	533	4	BI499160	BI499160	ie27d02.y
1254	57	1.8	815	4	BI689717	BI689717	603316221
1255	57	1.8	945	7	CF579434	CF579434	AGENCOURT
1256	56.8	1.8	774	7	CN539668	CN539668	UI-M-HU0-
1257	56.8	1.8	884	2	BE728944	BE728944	601562382
1258	56.8	1.8	917	4	BI913405	BI913405	603179004
1259	56.6	1.8	148	2	BB225254	BB225254	BB225254
1260	56.6	1.8	618	7	CN429152	CN429152	170006000
1261	56.6	1.8	624	6	CB527987	CB527987	UI-M-FY0-
c1262	56.4	1.8	148	2	AW045210	AW045210	UI-M-BH1-

1263	56.4	1.8	561	1	AA929737	AA929737	vz05h07.r
c1264	56.4	1.8	576	2	BE831264	BE831264	PM2-MT004
1265	56.4	1.8	589	7	CF179045	CF179045	813129 MA
1266	56.4	1.8	907	7	CF583319	CF583319	AGENCOURT
c1267	56.2	1.8	117	2	BF470020	BF470020	UI-M-BH3-
1268	56.2	1.8	222	2	BB548578	BB548578	BB548578
1269	56.2	1.8	794	9	CL640418	CL640418	G074D03 G
1270	56	1.8	822	5	BU208115	BU208115	603952728
1271	55.8	1.8	656	6	CD628627	CD628627	56097394H
1272	55.8	1.8	670	1	AL870127	AL870127	AL870127
c1273	55.8	1.8	717	7	CK225357	CK225357	704281487
1274	55.8	1.8	1051	5	BQ898681	BQ898681	AGENCOURT
1275	55.6	1.8	510	1	AA823166	AA823166	vw41e06.r
1276	55.6	1.8	596	5	BP872160	BP872160	BP872160
1277	55.4	1.8	307	1	AA354547	AA354547	EST62826
1278	55.4	1.8	391	6	CB775786	CB775786	AMGNNUC:N
1279	55.4	1.8	575	7	CN685188	CN685188	E0204H04-
1280	55.4	1.8	599	5	BP218578	BP218578	BP218578
1281	55.4	1.8	637	1	AU135310	AU135310	AU135310
1282	55.2	1.8	258	1	AA601686	AA601686	no02b07.s
c1283	55.2	1.8	428	5	BX683168	BX683168	BX683168
1284	55.2	1.8	647	7	CK338348	CK338348	C0629B03-
1285	55.2	1.8	672	6	BY751398	BY751398	BY751398
1286	55.2	1.8	754	7	CN538762	CN538762	UI-M-HS0-
1287	55.2	1.8	1066	4	BG542239	BG542239	602571680
1288	55	1.7	469	4	BG348876	BG348876	de74a05.y
1289	55	1.7	546	9	CG594195	CG594195	OST252072
1290	54.6	1.7	683	5	BU269132	BU269132	603506561
1291	54.6	1.7	938	5	BU150466	BU150466	AGENCOURT
1292	54.4	1.7	486	2	BE982860	BE982860	UI-M-CG0p
1293	54.4	1.7	711	7	CK694093	CK694093	ZF101-P00
1294	54.4	1.7	745	5	BU345393	BU345393	603523405
c1295	54	1.7	195	1	AI030698	AI030698	UI-R-C0-j
1296	54	1.7	573	2	BF550969	BF550969	UI-R-C0-j
1297	54	1.7	598	6	CB434784	CB434784	611453 MA
1298	54	1.7	600	5	BU924827	BU924827	7102-54 M
1299	54	1.7	925	9	CNS0091P	AL053013	Drosophil
1300	54	1.7	1106	6	CD498549	CD498549	CDA34-C01
1301	53.8	1.7	347	7	CN335013	CN335013	170005360
1302	53.8	1.7	598	4	BI908590	BI908590	603069993
1303	53.8	1.7	731	7	CR769103	CR769103	DKFZp469L
1304	53.6	1.7	651	6	BY722642	BY722642	BY722642
1305	53.4	1.7	1075	5	BM918793	BM918793	AGENCOURT
c1306	53.4	1.7	1462	3	CR715185	CR715185	Tetraodon
1307	53.2	1.7	562	7	CO322494	CO322494	EK188241.
1308	53.2	1.7	595	1	AL876266	AL876266	AL876266
1309	53.2	1.7	785	7	CO428820	CO428820	UI-M-HX0-
1310	53.2	1.7	987	9	CNS00418	AL066537	Drosophil
1311	52.8	1.7	345	4	BG148558	BG148558	uu80g02.y
1312	52.8	1.7	488	2	BF773594	BF773594	283122 MA
c1313	52.8	1.7	519	6	CB435264	CB435264	615337 MA
1314	52.8	1.7	787	4	BG783400	BG783400	SEAUMC003
1315	52.8	1.7	809	5	BU232264	BU232264	603410226
1316	52.6	1.7	442	7	CK392174	CK392174	K0842D11-
c1317	52.6	1.7	493	4	BG009731	BG009731	QV1-GN031
1318	52.6	1.7	564	2	AW659026	AW659026	95939 MAR
1319	52.6	1.7	626	1	AU137591	AU137591	AU137591

c1320	52.6	1.7	760	5	BX919359	BX919359	BX919359
1321	52.6	1.7	787	5	BU610933	BU610933	UI-M-FC0-
1322	52.6	1.7	817	4	BG342624	BG342624	602374614
1323	52.6	1.7	870	5	BU612231	BU612231	UI-M-EW0-
1324	52.6	1.7	2307	9	AY407762	AY407762	Mus muscu
1325	52.4	1.7	428	4	BI882131	BI882131	fm85b03.x
1326	52.4	1.7	525	2	BE260428	BE260428	601150894
1327	52.4	1.7	621	4	BI066930	BI066930	pgfln.pk0
1328	52.4	1.7	688	2	BE385519	BE385519	601278033
1329	52.4	1.7	699	6	CA327319	CA327319	UI-M-FY0-
1330	52.4	1.7	704	4	BG829860	BG829860	602764154
1331	52.4	1.7	927	5	BU148244	BU148244	AGENCOURT
1332	52.4	1.7	938	4	BG830609	BG830609	602767211
1333	52.2	1.7	387	5	BY093485	BY093485	BY093485
1334	52.2	1.7	740	4	BG831840	BG831840	602765483
1335	52.2	1.7	938	4	BG422234	BG422234	602446867
1336	52.2	1.7	962	4	BG324610	BG324610	602422587
1337	52	1.7	391	4	BJ620346	BJ620346	BJ620346
1338	52	1.7	479	4	BG010829	BG010829	IL5-GN024
1339	52	1.7	814	7	CK476539	CK476539	AGENCOURT
1340	52	1.7	2411	6	CB605722	CB605722	AMGNNUC:M
1341	51.8	1.6	576	4	BI067451	BI067451	pgfln.pk0
1342	51.8	1.6	687	4	BI916243	BI916243	603178146
1343	51.8	1.6	751	6	CA317826	CA317826	UI-M-FW0-
1344	51.6	1.6	588	5	BP218616	BP218616	BP218616
1345	51.6	1.6	761	7	CO734982	CO734982	SLLE04c10
1346	51.6	1.6	835	7	CO733414	CO733414	SLLT02c05
c1347	51.4	1.6	73	6	CD631367	CD631367	56027839H
1348	51.4	1.6	321	7	CO291094	CO291094	EK076120.
1349	51.4	1.6	367	6	CD371550	CD371550	UI-R-GO0-
1350	51.4	1.6	533	5	BU484169	BU484169	603469842
1351	51.4	1.6	647	4	BI067436	BI067436	pgfln.pk0
1352	51.4	1.6	743	6	CA326974	CA326974	UI-M-FY0-
1353	51.4	1.6	802	5	BU613129	BU613129	UI-M-EW0-
1354	51.4	1.6	1929	9	AY403444	AY403444	Pan trogl
1355	51.2	1.6	397	6	CB772279	CB772279	AMGNNUC:M
1356	51.2	1.6	582	5	BP349308	BP349308	BP349308
c1357	51.2	1.6	659	1	AI651838	AI651838	wb55h11.x
1358	51.2	1.6	675	2	BF707801	BF707801	A379_LE A
1359	51.2	1.6	728	1	AU137554	AU137554	AU137554
1360	51.2	1.6	748	1	AU136052	AU136052	AU136052
1361	51.2	1.6	773	5	BU515916	BU515916	AGENCOURT
1362	51.2	1.6	925	4	BG324814	BG324814	602423928
1363	51.2	1.6	948	4	BG325041	BG325041	602423476
1364	51	1.6	478	7	CN290121	CN290121	170005319
1365	51	1.6	563	4	BI791273	BI791273	id03h12.y
1366	51	1.6	755	1	AU137539	AU137539	AU137539
1367	51	1.6	774	7	CN537492	CN537492	UI-M-HS0-
1368	51	1.6	804	7	CO430718	CO430718	UI-M-HX0-
1369	51	1.6	2227	9	AY403443	AY403443	Homo sapi
1370	51	1.6	2596	3	AK053115	AK053115	Mus muscu
1371	50.8	1.6	650	7	CR429569	CR429569	CR429569
1372	50.8	1.6	671	6	CD295461	CD295461	StrPu691.
1373	50.8	1.6	760	2	BF181876	BF181876	601805303
1374	50.4	1.6	604	4	BI183160	BI183160	UNL-P-FN-
1375	50.2	1.6	283	7	CF136469	CF136469	UI-HF-BN0
1376	50.2	1.6	475	9	CL212177	CL212177	G033C05 G

1377	50.2	1.6	836	7	CK600018	CK600018	AGENCOURT
1378	50	1.6	505	2	BE487489	BE487489	176253 BA
1379	50	1.6	701	6	CB245456	CB245456	UI-M-FY0-
1380	50	1.6	735	1	AU140116	AU140116	AU140116
1381	49.8	1.6	519	4	BM741971	BM741971	K-EST0014
1382	49.8	1.6	805	5	BX844812	BX844812	BX844812
1383	49.6	1.6	300	7	CN255485	CN255485	170004251
1384	49.6	1.6	410	6	CB803735	CB803735	AMGNNUC:N
1385	49.6	1.6	549	6	CB614718	CB614718	AMGNNUC:N
1386	49.6	1.6	580	5	BU432018	BU432018	603836176
1387	49.6	1.6	612	7	CN951333	CN951333	Ha_mx0_46
1388	49.6	1.6	773	4	BI218305	BI218305	602934473
1389	49.4	1.6	410	6	CB153520	CB153520	K-EST0210
c1390	49.4	1.6	423	4	BI058070	BI058070	PM4-GN050
1391	49.4	1.6	516	6	CD619063	CD619063	56053362H
1392	49.4	1.6	516	6	CD619065	CD619065	56053454H
c1393	49.4	1.6	538	6	CD619064	CD619064	56053362J
c1394	49.4	1.6	550	6	CD619062	CD619062	56053346J
c1395	49.4	1.6	551	6	CD619060	CD619060	56053340J
c1396	49.4	1.6	552	6	CD619066	CD619066	56053454J
1397	49.4	1.6	559	6	CA872840	CA872840	K0920H08-
1398	49.4	1.6	595	5	BP271999	BP271999	BP271999
1399	49.4	1.6	688	4	BI552143	BI552143	603195086
1400	49.4	1.6	749	9	CNS02V9F	AL215484	Tetraodon
1401	49.4	1.6	766	4	BG825242	BG825242	602747664
1402	49.4	1.6	771	4	BI859915	BI859915	603386049
1403	49.4	1.6	910	9	CNS033DR	AL226008	Tetraodon
1404	49.2	1.6	542	4	BM740534	BM740534	K-EST0011
1405	49.2	1.6	544	4	BM766233	BM766233	K-EST0048
1406	49.2	1.6	626	4	BM740685	BM740685	K-EST0012
c1407	49.2	1.6	897	9	CG766342	CG766342	TcB48.4_B
c1408	49.2	1.6	898	9	CG770102	CG770102	TcB51.2_A
c1409	49.2	1.6	901	5	BQ433090	BQ433090	AGENCOURT
1410	49.2	1.6	904	5	BQ735037	BQ735037	AGENCOURT
1411	49.2	1.6	1177	5	BM906470	BM906470	AGENCOURT
1412	49.2	1.6	1309	5	BU541920	BU541920	AGENCOURT
c1413	49	1.6	293	6	CD631363	CD631363	56027739H
c1414	49	1.6	695	7	CK225361	CK225361	704197850
1415	49	1.6	1161	3	CR679362	CR679362	Tetraodon
c1416	48.8	1.6	372	1	AA984436	AA984436	am86d04.s
1417	48.8	1.6	412	6	CB801382	CB801382	AMGNNUC:M
1418	48.8	1.6	473	8	AQ603447	AQ603447	HS_2126_A
1419	48.8	1.6	610	2	BB613257	BB613257	BB613257
1420	48.8	1.6	726	7	CN042616	CN042616	v11_p43_g
1421	48.6	1.5	431	6	CB757701	CB757701	AMGNNUC:M
1422	48.6	1.5	702	4	BI771035	BI771035	603055382
1423	48.6	1.5	1809	3	AK051165	AK051165	Mus muscu
1424	48.6	1.5	3317	3	AK052671	AK052671	Mus muscu
1425	48.6	1.5	3672	3	AK028900	AK028900	Mus muscu
1426	48.6	1.5	4248	3	AK031704	AK031704	Mus muscu
1427	48.4	1.5	416	5	BY224521	BY224521	BY224521
1428	48.4	1.5	539	1	AL918018	AL918018	AL918018
1429	48.2	1.5	428	6	CB794320	CB794320	AMGNNUC:N
1430	48.2	1.5	640	6	CA334086	CA334086	NISC_ls05
1431	48.2	1.5	876	6	CA489866	CA489866	AGENCOURT
1432	48	1.5	384	6	CB703233	CB703233	AMGNNUC:N
1433	48	1.5	569	4	BI775284	BI775284	467707 MA

1434	48	1.5	817	7	CF994909	CF994909	AGENCOURT
c1435	48	1.5	963	5	BX341410	BX341410	BX341410
1436	47.8	1.5	253	4	BF988853	BF988853	IL5-GN017
1437	47.8	1.5	254	4	BM030705	BM030705	495185 MA
1438	47.8	1.5	406	6	CB808351	CB808351	AMGNNUC:S
c1439	47.8	1.5	420	2	AW803853	AW803853	IL2-UM008
c1440	47.8	1.5	537	6	CB717637	CB717637	AMGNNUC:U
1441	47.8	1.5	633	7	CN295126	CN295126	170005326
1442	47.8	1.5	975	2	BF101157	BF101157	601754732
1443	47.6	1.5	619	4	BI648895	BI648895	603275856
1444	47.6	1.5	709	6	CD348531	CD348531	UI-M-FY0-
1445	47.6	1.5	777	5	BU708565	BU708565	UI-M-FI0-
c1446	47.6	1.5	796	1	AL561140	AL561140	AL561140
1447	47.6	1.5	1911	9	AY403382	AY403382	Mus muscu
c1448	47.4	1.5	240	4	BI000873	BI000873	MR3-HN006
c1449	47.4	1.5	469	1	AA859662	AA859662	UI-R-E0-b
1450	47.4	1.5	613	5	BX271575	BX271575	BX271575
1451	47.2	1.5	645	4	BI066459	BI066459	pgfln.pk0
1452	47.2	1.5	654	2	BB037994	BB037994	BB037994
c1453	47.2	1.5	737	9	CR018931	CR018931	Reverse s
1454	47.2	1.5	775	5	BU703431	BU703431	UI-M-FO0-
1455	47.2	1.5	1023	6	CD245257	CD245257	AGENCOURT
c1456	47	1.5	367	5	BQ320183	BQ320183	PM4-CT082
1457	47	1.5	480	7	CR579310	CR579310	CR579310
1458	47	1.5	511	4	BI673056	BI673056	ft33e03.y
1459	47	1.5	516	6	CD619061	CD619061	56053346H
1460	47	1.5	543	1	AA940432	AA940432	vz48h07.r
1461	47	1.5	625	4	BI753404	BI753404	603026593
1462	47	1.5	834	7	CF149484	CF149484	AGENCOURT
1463	46.8	1.5	350	5	BY200122	BY200122	BY200122
1464	46.8	1.5	365	2	AW437778	AW437778	79230 MAR
1465	46.8	1.5	635	1	AL852575	AL852575	AL852575
c1466	46.8	1.5	741	2	BF232471	BF232471	de06c04.x
1467	46.8	1.5	932	9	CNS022IX	AL178242	Tetraodon
1468	46.8	1.5	950	5	BU175283	BU175283	AGENCOURT
c1469	46.8	1.5	1131	5	BM922197	BM922197	AGENCOURT
1470	46.6	1.5	533	1	AA175711	AA175711	ms97a05.r
1471	46.6	1.5	609	4	BI066327	BI066327	pgfln.pk0
1472	46.6	1.5	641	6	BY728676	BY728676	BY728676
1473	46.6	1.5	688	4	BG700674	BG700674	602682306
1474	46.4	1.5	395	6	CB773879	CB773879	AMGNNUC:N
c1475	46.4	1.5	678	9	CC569313	CC569313	CH240_444
1476	46.4	1.5	957	4	BG261855	BG261855	602373655
1477	46.4	1.5	971	4	BG342228	BG342228	602374305
c1478	46.4	1.5	985	5	BX402983	BX402983	BX402983
1479	46.4	1.5	994	5	BQ929877	BQ929877	AGENCOURT
1480	46.2	1.5	564	7	CK635703	CK635703	UI-M-HN0-
1481	46.2	1.5	570	2	BE033028	BE033028	133242 MA
1482	46.2	1.5	590	9	AY420627	AY420627	Homo sapi
1483	46.2	1.5	594	7	CN409468	CN409468	170004276
1484	46.2	1.5	624	2	AW328571	AW328571	ds03dl2.x
1485	46.2	1.5	634	5	BM951500	BM951500	UI-M-EG0-
1486	46.2	1.5	650	7	CF746951	CF746951	UI-M-HE0-
1487	46.2	1.5	658	7	CN409465	CN409465	170005325
1488	46.2	1.5	678	7	CN409457	CN409457	170004177
1489	46.2	1.5	732	7	CN409463	CN409463	170005325
1490	46.2	1.5	732	7	CN531114	CN531114	UI-M-HO0-

1491	46.2	1.5	741	7	CF730435	CF730435	UI-M-GZ0-
1492	46.2	1.5	778	7	CF736303	CF736303	UI-M-HD0-
1493	46	1.5	394	6	CB776561	CB776561	AMGNNUC:S
c1494	46	1.5	428	1	AI458053	AI458053	tj66h10.x
1495	46	1.5	528	2	BE334076	BE334076	us29e10.y
1496	46	1.5	575	5	BP338720	BP338720	BP338720
1497	46	1.5	714	7	CR789306	CR789306	DKFZp4590
1498	46	1.5	2775	3	AK077021	AK077021	Mus muscu
1499	45.8	1.5	372	2	BF443919	BF443919	261588 MA
1500	45.8	1.5	375	6	CB691762	CB691762	AMGNNUC:M

ALIGNMENTS

RESULT 1

CR623694

LOCUS CR623694 3005 bp mRNA linear HTC 21-JUL-2004

DEFINITION full-length cDNA clone CSODL005YC17 of B cells (Ramos cell line)
Cot 25-normalized of Homo sapiens (human).

ACCESSION CR623694

VERSION CR623694.1 GI:50504501

KEYWORDS HTC; CNSLT_cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3005)

AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600
Faraday Avenue

REFERENCE 2 (bases 1 to 3005)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES Location/Qualifiers

source

1. .3005

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODL005YC17"

/tissue_type="B cells (Ramos cell line) Cot 25-normalized"

/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 95.6%; Score 3005; DB 3; Length 3005;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	99	CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC	158
Db	1	CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC	60
Qy	159	TTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCC	218
Db	61	TTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCC	120
Qy	219	ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG	278
Db	121	ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG	180
Qy	279	AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG	338
Db	181	AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG	240
Qy	339	GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGTCCCCAGGCTAAAG	398
Db	241	GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGTCCCCAGGCTAAAG	300
Qy	399	AACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAAGAAGAAG	458
Db	301	AACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAAGAAGAAG	360
Qy	459	AGCAATGAGACACAGTGTTCACCTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCAT	518
Db	361	AGCAATGAGACACAGTGTTCACCTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCAT	420
Qy	519	CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGAT	578
Db	421	CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGAT	480
Qy	579	TCCTACCTGTTGCCCCATCTCGGAGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCTTT	638
Db	481	TCCTACCTGTTGCCCCATCTCGGAGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCTTT	540
Qy	639	GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG	698
Db	541	GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG	600
Qy	699	AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC	758
Db	601	AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC	660
Qy	759	AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT	818
Db	661	AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT	720
Qy	819	TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG	878
Db	721	TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG	780
Qy	879	AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG	938
Db	781	AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG	840

Qy	939	CTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAG	998
Db	841	CTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAG	900
Qy	999	CTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCC	1058
Db	901	CTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCC	960
Qy	1059	CACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTT	1118
Db	961	CACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTT	1020
Qy	1119	TGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAAC	1178
Db	1021	TGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAAC	1080
Qy	1179	AAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGT	1238
Db	1081	AAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGT	1140
Qy	1239	TGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATG	1298
Db	1141	TGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATG	1200
Qy	1299	GATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT	1358
Db	1201	GATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT	1260
Qy	1359	GCAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACC	1418
Db	1261	GCAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACC	1320
Qy	1419	ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA	1478
Db	1321	ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA	1380
Qy	1479	GAGATTACAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAG	1538
Db	1381	GAGATTACAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAG	1440
Qy	1539	GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGT	1598
Db	1441	GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGT	1500
Qy	1599	GTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCT	1658
Db	1501	GTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCT	1560
Qy	1659	GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACCTCTGGAAGCAGGACATG	1718
Db	1561	GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACCTCTGGAAGCAGGACATG	1620
Qy	1719	GAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT	1778
Db	1621	GAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT	1680

Qy	1779	CAGAGCCGCCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTC	1838
Db	1681	CAGAGCCGCCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTC	1740
Qy	1839	CCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTC	1898
Db	1741	CCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTC	1800
Qy	1899	CCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTT	1958
Db	1801	CCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTT	1860
Qy	1959	GGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTAC	2018
Db	1861	GGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTAC	1920
Qy	2019	TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAAGTGGCAGGCATCCCCCGG	2078
Db	1921	TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAAGTGGCAGGCATCCCCCGG	1980
Qy	2079	GAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAG	2138
Db	1981	GAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAG	2040
Qy	2139	TCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCC	2198
Db	2041	TCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCC	2100
Qy	2199	CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGC	2258
Db	2101	CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGC	2160
Qy	2259	TGTGAGACCCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCT	2318
Db	2161	TGTGAGACCCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCT	2220
Qy	2319	CCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACT	2378
Db	2221	CCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACT	2280
Qy	2379	GAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGG	2438
Db	2281	GAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGG	2340
Qy	2439	CTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTC	2498
Db	2341	CTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTC	2400
Qy	2499	CCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAG	2558
Db	2401	CCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAG	2460
Qy	2559	CAGTCTGCCTCCCCATATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGG	2618
Db	2461	CAGTCTGCCTCCCCATATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGG	2520
Qy	2619	GGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGT	2678

Db	2521	GGGCTACCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGT	2580
Qy	2679	TCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGC	2738
Db	2581	TCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGC	2640
Qy	2739	CTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGC	2798
Db	2641	CTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGC	2700
Qy	2799	CACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCAG	2858
Db	2701	CACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCAG	2760
Qy	2859	GGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCA	2918
Db	2761	GGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCA	2820
Qy	2919	GGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAGTTGGGGCAGACTCTGAT	2978
Db	2821	GGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAGTTGGGGCAGACTCTGAT	2880
Qy	2979	CCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAG	3038
Db	2881	CCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAG	2940
Qy	3039	CTGACCCCTTCACCTCTCCCCCTCCCTTTTCCCTTTGTTTTGGGATTTCAGAAAACCTGCTTG	3098
Db	2941	CTGACCCCTTCACCTCTCCCCCTCCCTTTTCCCTTTGTTTTGGGATTTCAGAAAACCTGCTTG	3000
Qy	3099	TCAGA 3103	
Db	3001	TCAGA 3005	

RESULT 2
HSM807023

LOCUS	HSM807023	3151 bp	mRNA	linear	HTC 22-SEP-2004
DEFINITION	Homo sapiens mRNA; cDNA DKFZp686D04248 (from clone DKFZp686D04248).				
ACCESSION	BX640891				
VERSION	BX640891.1 GI:34365195				
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 3151)				
AUTHORS	Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.				
CONSRM	The German cDNA Consortium				
TITLE	Direct Submission				
JOURNAL	Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY				
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;				

sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686D04248) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686D04248>
 Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

```

FEATURES
    source          1. .3151
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="RZPD:DKFZp686D04248Q"
                    /db_xref="taxon:9606"
                    /clone="DKFZp686D04248"
                    /tissue_type="salivary gland"
                    /clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
                    DH10B; sites SfiIA + SfiIB"
                    /dev_stage="adult"
                    /note="Semaphorin B, differentially spliced, alternative
                    start"
    gene            1. .3151
                    /gene="DKFZp686D04248"
    CDS              217. .2388
                    /gene="DKFZp686D04248"
                    /codon_start=1
                    /product="hypothetical protein"
                    /protein_id="CAE45942.1"
                    /db_xref="GI:34365196"
                    /db_xref="UniProt/TrEMBL:Q6MZT6"
                    /translation="MPRVRYAGDERRALSFFHQKGLQDFDTLLLSGDGNTLYVGARE
                    AILALDIQDPGVPRLNMI PWPASDRKKSECAFKKSNETQCENFIRVLVSYNVTHLY
                    TCGTFAFSPACTFIELQDSYLLPI SEDKVMGKGQSPFDPAHKHTAVLVDGMLYSGTM
                    NNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAI PSTQVVYFFFEETASEFDF
                    FERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPQQLPFNVIRHAVLLPADS
                    PTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
                    NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHS
                    HLMYLGTTPGSLHKAVVSGDSSAHLVEEIQLFDPDPEPVRNLQLAPTQGAVFVGFSGG
                    VWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWA
                    CASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASST
                    VYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVK
                    VPLTRVSGGAALAAQSYWPHFVTVTVLFAVLVSGALIILVASPLRALRARGKVQGCCE
                    TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA"

```

ORIGIN

Query Match 93.1%; Score 2927.6; DB 3; Length 3151;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2933; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

Qy      202 GAGGCGGGCAGGGGCCCATGCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCAC 261
          | ||| |          |||
Db      200 GTGGCTGAGCATGGCCCATGCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCAC 259

Qy      262 TTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATG 321
          |||
Db      260 TTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATG 319

```

Qy	322	GAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAG	381
Db	320	GAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAG	379
Qy	382	GGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAAT	441
Db	380	GGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAAT	439
Qy	442	GTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGT	501
Db	440	GTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGT	499
Qy	502	CTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCT	561
Db	500	CTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCT	559
Qy	562	TCATTGAACTTCAAGATTCCCTACCTGTTGCCATCTCGGAGGACAAGGTCATGGAGGGAA	621
Db	560	TCATTGAACTTCAAGATTCCCTACCTGTTGCCATCTCGGAGGACAAGGTCATGGAGGGAA	619
Qy	622	AAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGC	681
Db	620	AAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGC	679
Qy	682	TCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGG	741
Db	680	TCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGG	739
Qy	742	GATCCCAGCCTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCT	801
Db	740	GATCCCAGCCTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCT	799
Qy	802	TTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCG	861
Db	800	TTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCG	859
Qy	862	AGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACG	921
Db	860	AGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACG	919
Qy	922	TGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCT	981
Db	920	TGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCT	979
Qy	982	GCACCCAGCCGGGGCAGCTGCCCTTCAACGTATCCGCCACGCGGTCTGCTCCCCGCCG	1041
Db	980	GCACCCAGCCGGGGCAGCTGCCCTTCAACGTATCCGCCACGCGGTCTGCTCCCCGCCG	1039
Qy	1042	ATTCTCCACAGCTCCCCACATCTACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGA	1101
Db	1040	ATTCTCCACAGCTCCCCACATCTACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGA	1099
Qy	1102	CCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGA	1161
Db	1100	CCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGA	1159
Qy	1162	AATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCA	1221

Db	1160	 AATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGGCCCTGAGACCA	1219
Qy	1222	 ACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGA	1281
Db	1220	 ACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGA	1279
Qy	1282	 AGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCG	1341
Db	1280	 AGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCG	1339
Qy	1342	 TGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTG	1401
Db	1340	 TGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTG	1399
Qy	1402	 TCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCA	1461
Db	1400	 TCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCA	1459
Qy	1462	 GTGCTCATCTGGTGGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGC	1521
Db	1460	 GTGCTCATCTGGTGGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGC	1519
Qy	1522	 AGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCCTGGAGGGTGC	1581
Db	1520	 AGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCCTGGAGGGTGC	1579
Qy	1582	 CCCAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCC	1641
Db	1580	 CCCAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCC	1639
Qy	1642	 ACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACT	1701
Db	1640	 ACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACT	1699
Qy	1702	 CCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGA	1761
Db	1700	 CCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGA	1759
Qy	1762	 GCAGGAGCCTTCGGCCTCAGAGCCGCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCA	1821
Db	1760	 GCAGGAGCCTTCGGCCTCAGAGCCGCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCA	1819
Qy	1822	 ACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGCCCTCTTATTATTGGAGTC	1881
Db	1820	 ACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGCCCTCTTATTATTGGAGTC	1879
Qy	1882	 ATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGA	1941
Db	1880	 ATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGA	1939
Qy	1942	 TAGTGCAGGATGGAGTTGGGGGTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCAT	2001
Db	1940	 TAGTGCAGGATGGAGTTGGGGGTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCAT	1999
Qy	2002	 ACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCTGGCCCTGGATCCTGAAC	2061

Db	2000	ACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAAC	2059
Qy	2062	TGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCG	2121
Db	2060	TGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCG	2119
Qy	2122	CCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCCTCTTTGCCT	2181
Db	2120	CCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCCTCTTTGCCT	2179
Qy	2182	TAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTC	2241
Db	2180	TAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTC	2239
Qy	2242	GGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAG	2301
Db	2240	GGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAG	2299
Qy	2302	AGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACA	2361
Db	2300	AGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACA	2359
Qy	2362	ACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAG	2421
Db	2360	ACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAG	2419
Qy	2422	GCACCTGGCCATGCTGGCTGGGCGGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCAC	2481
Db	2420	GCACCTGGCCATGCTGGCTGGGCGGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCAC	2479
Qy	2482	AAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTC	2541
Db	2480	AAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTC	2539
Qy	2542	AGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGA	2601
Db	2540	AGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGA	2599
Qy	2602	GCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCT	2661
Db	2600	GCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCT	2659
Qy	2662	GGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGA	2721
Db	2660	GGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGA	2719
Qy	2722	GACCCATAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACA	2781
Db	2720	GACCCATAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACA	2779
Qy	2782	ATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCA	2841
Db	2780	ATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCA	2839
Qy	2842	ACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCG	2901
Db	2840	ACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCG	2899

Qy 2902 TGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCTTCAG 2961
 |||
 Db 2900 TGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCTTCAG 2959

Qy 2962 TTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCT 3021
 |||
 Db 2960 TTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCT 3019

Qy 3022 TCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGG 3081
 |||
 Db 3020 TCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGG 3079

Qy 3082 ATTCAGAAAAGCTGCTTGTCTGAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAA 3141
 |||
 Db 3080 ATTCAGAAAAGCTGCTTGTCTGAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAA 3139

Qy 3142 AA 3143
 ||
 Db 3140 AA 3141

RESULT 3

AY402621

LOCUS AY402621 2172 bp DNA linear GSS 12-DEC-2003

DEFINITION Homo sapiens HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY402621

VERSION AY402621.1 GI:39758607

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2172)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2172)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .2172

/organism="Homo sapiens"

/mol_type="genomic DNA"

```

gene          /db_xref="taxon:9606"
              <1..>2172
              /locus_tag="HCM1285"
ORIGIN
Query Match      59.6%; Score 1874; DB 9; Length 2172;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1874; Conservative 0; Mismatches 298; Indels 0; Gaps 0;

Qy      105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1   ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 60

Qy      165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGGCCCATGCCC 224
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGGCCCATGCCC 120

Qy      225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy      285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 240

Qy      345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCAGGC'TAAAGAACATG 404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCAGGC'TAAAGAACATG 300

Qy      405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy      465 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 420

Qy      525 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGACCTTCATTGAAC'TTCAAGATTCCTAC 584
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGACCTTCATTGAAC'TTCAAGATTCCTAC 480

Qy      585 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCC'TTTGACCCC 644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCC'TTTGACCCC 540

Qy      645 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 600

Qy      705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCC'TCAAGACC 764
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCC'TCAAGACC 660

Qy      765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GACAACTTCCTCCGCTGGCTGCATC'NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720

```

[illegible]

Db	1561		CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG	1620
Qy	1725		GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1784
Db	1621		GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1680
Qy	1785		CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1844
Db	1681		CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1740
Qy	1845		CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1904
Db	1741		CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1800
Qy	1905		GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1964
Db	1801		GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1860
Qy	1965		CTCTACCAAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	2024
Db	1861		CTCTACCAAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	1920
Qy	2025		GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT	2084
Db	1921		GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT	1980
Qy	2085		GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCTAC	2144
Db	1981		GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCTAC	2040
Qy	2145		TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC	2204
Db	2041		TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC	2100
Qy	2205		ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG	2264
Db	2101		ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG	2160
Qy	2265		ACCCTGCGCCCT	2276
Db	2161		ACCCTGCGCCCT	2172

RESULT 4

AY402622

LOCUS AY402622 2133 bp DNA linear GSS 12-DEC-2003
 DEFINITION Pan troglodytes HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY402622

VERSION AY402622.1 GI:39758608

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 2133)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2133)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .2133

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

gene <1. .>2133

/locus_tag="HCM1285"

ORIGIN

Query Match 56.2%; Score 1765.4; DB 9; Length 2133;

Best Local Similarity 82.9%; Pred. No. 0;

Matches 1769; Conservative 0; Mismatches 364; Indels 0; Gaps 0;

Qy 105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164

|||||

Db 1 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 60

Qy 165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 224

|||||

Db 61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGANNCGGGCAGGGGCCCATGCCC 120

Qy 225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284

|||||

Db 121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy 285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344

|||||

Db 181 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 240

Qy 345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGTCCCCAGGCTAAAGAACATG 404

|||||

Db 241 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGTCCCCAGGCTAAAGAACATG 300

Qy 405 ATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464

|||||

Db 301 ATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy 465 GAGACACAGTGTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524

|||||

Db		361 GAGACACAGTGTTCCTCAACTTCATCCGTTGCTCCTGGTTTTCTTTACAATGTCAACCATCTCTAC	420
Qy	525 ACCTGCGGCACCTTCGCCCTTCAGCCCCTGCTTGTAACCTTCATTGAACCTCAAGATTCCTAC	584	
Db	421 ACCTGCGGCACCTTCGCCCTTCAGCCCCTGCTTGTAACCTTCATTGAACCTCAAGATTCCTAC	480	
Qy	585 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAAGGCCAAAGCCCCCTTTGACCCCC	644	
Db	481 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAAGGCCAAAGCCCCCTTTGACCCCC	540	
Qy	645 GCTCACAAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC	704	
Db	541 GCTCACAAAGCATACGGCTGTCTTGGTGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	600	
Qy	705 TTCCTGGGACAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCTCAAGACC	764	
Db	601 NTCCTGGGACAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCTCAAGACC	660	
Qy	765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC	824	
Db	661 GACAACTTCCTCCGCTGGCTGCATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	720	
Qy	825 CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC	884	
Db	721 NN	780	
Qy	885 CACACATCGCGGGTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG	944	
Db	781 NN	840	
Qy	945 AAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC	1004	
Db	841 NN	900	
Qy	1005 TTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC	1064	
Db	901 NN	960	
Qy	1065 TACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGACAGGAGCTCTGCGGTTTGTGCC	1124	
Db	961 NNNNNNNNNNNNNNNNNNNNNNNNGCAGGTTGGCGGGACAGGAGCTCTGCGGTTTGTGCC	1020	
Qy	1125 TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA	1184	
Db	1021 TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA	1080	
Qy	1185 ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGCCAGGCAGTTGCTCA	1244	
Db	1081 ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGCCAGGCAGTTGCTCA	1140	
Qy	1245 GTGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG	1304	
Db	1141 GTGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG	1200	
Qy	1305 CAAGTGGTGGGGACGCCCCCTGCTGGTGAATCTGGCGTGGAGTATACACGGCTTGACAGTG	1364	
Db	1201 CAGGTGGTAGGGACGCCCCCTGCTGGTGAATCTGGCGTGGAGTATACACGGCTTGACAGTG	1260	

Qy	1365	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA	1424
Db	1261	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA	1320
Qy	1425	GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT	1484
Db	1321	GGGTCGNTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGANNNNTT	1380
Qy	1485	CAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCA	1544
Db	1381	CAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCA	1440
Qy	1545	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACGTAGTGTCTAT	1604
Db	1441	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACGTAGTGTCTAT	1500
Qy	1605	GAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGCCTGGGACCTGAGTCC	1664
Db	1501	GAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGCCTGGGATCCTGAGTCC	1560
Qy	1665	CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG	1724
Db	1561	CGAACCTGTTGCCTCCTNNNNNNNNNNNNNGAACTCCTGGAAGCAGGACATGGAGCGG	1620
Qy	1725	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1784
Db	1621	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1680
Qy	1785	CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1844
Db	1681	CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGAGNTCCCCTGC	1740
Qy	1845	CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1904
Db	1741	CCCCACCTGTCAGCCTTGGCCTCTTACTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1800
Qy	1905	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1964
Db	1801	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1860
Qy	1965	CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	2024
Db	1861	CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	1920
Qy	2025	GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT	2084
Db	1921	GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT	1980
Qy	2085	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCCTAC	2144
Db	1981	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCCTAC	2040
Qy	2145	TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATC	2204
Db	2041	TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATC	2100

REFERENCE 6 (bases 1 to 3206)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1..3206 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:6030492A12" /db_xref="taxon:10090" /clone="6030492A12" /sex="male" /tissue_type="testis" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="13 days embryo"

misc_feature 224..2507 /note="putative sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A (MGD|MGI:107560, GB|NM_013658, evidence: BLASTN, 99%, match=2517)"

polyA_signal 3181..3186 /note="putative"

polyA_site 3206 /note="putative"

ORIGIN

Query Match 55.6%; Score 1747.4; DB 3; Length 3206;
 Best Local Similarity 76.7%; Pred. No. 0;
 Matches 2355; Conservative 0; Mismatches 621; Indels 95; Gaps 14;

Qy 75 GAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCC 134
 || | ||||| ||| ||||| ||||| ||| ||||| |||||
 Db 194 GAACCATCTGGTGACCATCTCAGGCTGACCATGGCCCTACCATCCCTGGGCCAGGACTCA 253

Qy 135 TGGAGCCTCCTGGGCCTTTTCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACC 194
 ||||| ||||| | ||| ||||| ||| | ||||| | | | | |
 Db 254 TGGAGTCTCCTGCGTGTTTTTTCTTCCAACCTCTTCTGCTGCCATCACTGCCACCTGCT 313

Qy 195 GCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGT 254
 | ||| || || ||||| ||||| ||||| ||||| ||||| ||| |
 Db 314 TCTGGGACTGGTGGTCAGGGGCCCATGCCCAGAGTCAAATACCATGCTGGAGACGGGCAC 373

Qy 255 AGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGT 314
 ||||| || ||||| ||||| || || ||||| || ||||| ||||| |||||
 Db 374 AGGGCCCTCAGCTTCTTCCAACAAAAAGGCCTCCGAGACTTTGACACGCTGCTCCTGAGT 433

Qy 315 GGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAG 374
 | ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 434 GACGATGGCAACACTCTCTATGTGGGGGCTCGAGAGGCCGTCTTGGCCTTGAATATCCAG 493

Qy 375 GATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAG 434
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 494 AACCAGGAATCCCAAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGAGAGAAAAAAG 553

Qy 435 AGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTC 494
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 554 ACCGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATTCGAGTC 613

Qy 495 CTGGTTTCTTACAATGTCAACCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCT 554
 ||||| ||||| ||||| || || ||||| ||||| || ||||| ||||| |||||
 Db 614 CTGGTCTCTTACAATGCTACTCACCTCTATGCCTGTGGGACCTTTGCCTTCAGCCCTGCC 673

Qy 555 TGTACCTTCATTGAACTTCAAGATTCCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATG 614
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 674 TGTACCTTCATTGAACTCCAAGATTCCCTCCTGTTGCCCATCTTGATAGACAAGGTCATG 733

Qy 615 GAGGGAAAAGGCCAAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGAT 674
 || || || ||||| ||||| ||||| || ||||| || ||||| ||||| |||||
 Db 734 GACGGGAAGGGCCAAAAGCCCCTTTGACCCCTGTTTCAAGCACACAGCTGTCTTGGTCGAT 793

Qy 675 GGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGC 734
 ||||| ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
 Db 794 GGGATGCTTTATTCCGGCACCATGAACAACTTCCTGGGCAGCGAGCCCATCCTGATGCGG 853

Qy 735 ACACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGAC 794
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 854 ACACTGGGATCCCAGCCTGTTCTCAAGACTGACATCTTCTTACGCTGGCTGCACGCGGAT 913

Qy 795 GCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACA 854
 ||||| ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
 Db 914 GCCTCCTTCGTGGCAGCCATTCCATCCACCCAGGTCGTCTATTTCTTCTTTGAGGAGACA 973

Qy 855 GCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAG 914
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 974 GCCAGCGAGTTTGACTTCTTTGAAGAGCTGTATATATCCAGGGTGGCTCAAGTCTGCAAG 1033

Qy 915 AATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCTTGAAGGCCAG 974

Db	1034	AACGACGTGGGCGGTGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTCAAAGCCCAG	1093
Qy	975	CTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGTCTC	1034
Db	1094	TTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCCGCCACGCGGTCTGTCTG	1153
Qy	1035	CCCGCCGATTCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTT	1094
Db	1154	CCCGCCGATTCTCCCTCTGTTTCCCGCATCTACGCAGTCTTTACCTCCCAGTGGCAGGTT	1213
Qy	1095	GGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTT	1154
Db	1214	GGCGGGACCAGGAGCTCAGCAGTCTGTGCCTTCTCTCTCACGGACATTGAGCGAGTCTTT	1273
Qy	1155	AAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGGCCCT	1214
Db	1274	AAAGGGAAGTACAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACTTACCGGGGCTCA	1333
Qy	1215	GAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACC	1274
Db	1334	GAGGTCAGCCCGAGGCAAGGCAGTTGCTCCATGGGCCCCCTCCTCTGACAAAGCCTTGACC	1393
Qy	1275	TTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAA	1334
Db	1394	TTCATGAAGGACCATTTCCTGATGGATGAGCACGTGGTAGGAACACCCCTGCTGGTGAAAG	1453
Qy	1335	TCTGGCGTGGAGTATACACGGCTTGACAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGC	1394
Db	1454	TCTGGTGTGGAGTACACACGGCTTGCTGTGGAGTCAGCTCGGGGCCTTGATGGGAGCAGC	1513
Qy	1395	CATCTTGTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGG	1454
Db	1514	CATGTGGTTCATGTATCTGGGTACCTCCACGGGGTCCCTGCACAAGGCTGTGGTGCCTCAG	1573
Qy	1455	GACAGCAGTGCTCATCTGGTGGAGAGATTGAGCTG-TTCCCTGACCCTGAACCTGTTTCG	1513
Db	1574	GACAGCAGTGCTTATCTCGTGGAGGAGATTGAGCTGAGCCCCCTGACTCTGAGCCTGTTTCG	1633
Qy	1514	CAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTG	1573
Db	1634	AAACCTGCAGCTGGCCCCCGCCAGGGTGCAGTGTTTGCAGGCTTCTCTGGAGGCATCTG	1693
Qy	1574	GAGGGTGTCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCG	1633
Db	1694	GAGAGTTCACAGGGCCAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCTTGCCAG	1753
Qy	1634	GGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAA	1693
Db	1754	GGACCCCTCACTGTGCCTGGGACCCTGAATCAAGACTCTGCAGCCTTCTGTCTGGCTCTAC	1813
Qy	1694	CCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGG	1753
Db	1814	C---AAGCCTTGAAGCAGGACATGGAACGCGGCAACCCGAGTGGGTATGCACCCGTGG	1870
Qy	1754	CCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGC	1813

Db 1871 CCCCATGGCCAGGAGCCCCCGGCGTCAGAGCCCCCTCAACTAATTAAAGAAGTCCTGAC 1930

Qy 1814 TGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTA 1873
 |||||

Db 1931 AGTCCCCAACTCCATCCTGGAGCTGCCCTGCCCCACCTGTCAGCACTGGCCTCTTACCA 1990

Qy 1874 TTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCT 1933
 |||||

Db 1991 CTGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGCTACCGTCTACAATGGCTCCCT 2050

Qy 1934 CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGG 1993
 |||||

Db 2051 CTTGCTGCTGCCGAGGATGGTGTGCGAGGCCTCTACCAGTGCTGTGGCGACTGAGAACGG 2110

Qy 1994 CTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGA 2053
 ||

Db 2111 CTACTCATACCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCAGCCCCTGGCGCTGGA 2170

Qy 2054 TCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGG 2113
 |||||

Db 2171 CCCTGAGCTGGCGGGCGTTCCCCGTGAGCGTGTGCAGGTCCCGCTGACCAGGGTCGGAGG 2230

Qy 2114 TGGGGCCGCCCTGGCTGCCCAGCAGTCCCTACTGGCCCCACTTTGTCACTGTCACTGTCCT 2173
 ||

Db 2231 CGGAGCTTCCATGGCTGCCCAGCGGTCCCTACTGGCCCCATTTCTCATCGTTACCGTCCT 2290

Qy 2174 CTTTGCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACT 2233
 ||

Db 2291 CCTGGCCATCGTGCTCCTGGGAGTGCTCACTCTCCTCCTCGCTTCCCCACTGGGGGCGCT 2350

Qy 2234 CCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGCTT 2293
 |||||

Db 2351 GCGGGCTCGGGGTAAGGTTTCAGGGCTGTGGGATGCTGCCCCCAGGGAAAAGGCTCCACT 2410

Qy 2294 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGA 2353
 |||||

Db 2411 GAGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGACGTAGA 2470

Qy 2354 CGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAACTCTAGGCACAGGCCGGGGCT- 2412
 ||

Db 2471 TGCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACAGGGACACAGATCCGCAGCTG 2530

Qy 2413 -GCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGGCCCAAGCACAGCCCTGACTAGGATG 2471
 ||

Db 2531 AGCAGAGCAAGCCACTGGCCTTGTTGGCTATGC----- 2563

Qy 2472 ACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACT 2531
 |||

Db 2564 ----CAGGCACAGTGCCACTCTGACCAGGGTAGGAGGCTCTCCTGCTAACGTGTGTCACT 2619

Qy 2532 GATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACC 2591
 |

Db 2620 TACAGCACCCAGTAGG-----TCCTCCCCTGTGGGACTCTCTTCTGCA 2662

Qy 2592 AAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATAT 2651
 |

Db 2663 AGCACATTGGGCTGTCT-----CCATACCTGTACTTGTGCTGTGAC 2703

Qy 2652 TGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAG 2711
 | | | | | | | | | | | | | | | | | | |
 Db 2704 AGGAAGAGCCAGACAGGTTTCTTTGATTTTGATTGACCCAAGAGCCCTCCTGTAACAAAC 2763
 Qy 2712 TGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAA 2771
 | | | | | | | | | | | | | | | | | | |
 Db 2764 GTGCTCCAGGAGACCATGAAAGGTGTGGCTGTCTGGGATTCTGTGGTGACAAAC-CTAAG 2822
 Qy 2772 CATCTAAACAATCATATGCTA-----ACATGCCACTCCTGGAAACTCCACTCT----G 2820
 | | | | | | | | | | | | | | | | | | |
 Db 2823 CATCCGAGCAAGCTGGGGCTATTCTGCAAACTCCATCCTGAACGCTGTCACCTCTAGAAG 2882
 Qy 2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAGGGATCTGCTCC 2879
 | | | | | | | | | | | | | | | | | | |
 Db 2883 CAGCTGCTGCTTTGAACACCAGCCACCCTCCTTCCCAAGAGTCTCTATGGAGTTGGCCC 2942
 Qy 2880 CTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTG 2939
 | | | | | | | | | | | | | | | | | | |
 Db 2943 CTTGTGTTTCCCTTTACCAGTCATGCCATACTGTTT---GGGAAGTCATCTCTGAAGTCTA 2999
 Qy 2940 ACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCT---TCTGCCCTGGC-AG 2995
 | | | | | | | | | | | | | | | | | | |
 Db 3000 ACCACCTTCCTTCTTGCTTCAGTTTGACAGATTGTTATTATTGTCTCTGCCCTGGCTAG 3059
 Qy 2996 AATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCT 3055
 | | | | | | | | | | | | | | | | | | |
 Db 3060 AATGGGGGGCATAATCTGAGCCTTGTTCCTTGTCCAGTGTGGCTGACCCCTTGACCTCTT 3119
 Qy 3056 CCCCTCCCTTTTCCCTTTGTTTGGGATTTCAGAAAACCTGCTTGTGACAGACTGTTTATTT 3115
 | | | | | | | | | | | | | | | | | | |
 Db 3120 --CCTTCCTCCTCCCTTTGTTTGGGATTTCAGAAAACCTGCTTGTGACAGACAATTTATTT 3177
 Qy 3116 TTTATTAAAAA 3126
 | | | | | | | | |
 Db 3178 TTTATTAAAAA 3188

RESULT 6

AK035918

LOCUS AK035918 3086 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630018D15 product:sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A, full insert sequence.

ACCESSION AK035918

VERSION AK035918.1 GI:26084904

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636
 REFERENCE 2
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 3086)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:<http://genome.gsc.riken.jp/>
URL:<http://fantom.gsc.riken.jp/>.

```

FEATURES             Location/Qualifiers
    source             1. .3086
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="C57BL/6J"
                        /db_xref="FANTOM_DB:9630018D15"
                        /db_xref="taxon:10090"
                        /clone="9630018D15"
                        /tissue_type="cerebellum"
                        /clone_lib="RIKEN full-length enriched mouse cDNA library"
                        /dev_stage="16 days neonate"
    misc_feature       59. .2388
                        /note="putative
                        sema domain, immunoglobulin domain (Ig), transmembrane
                        domain (TM) and short cytoplasmic domain, (semaphorin) 4A
                        (MGD|MGI:107560, GB|NM_013658, evidence: BLASTN, 99%,
                        match=2517)"
    polyA_signal       3062. .3067
                        /note="putative"
    polyA_site         3086
                        /note="putative"

```

ORIGIN

Query Match 54.1%; Score 1701.4; DB 3; Length 3086;
Best Local Similarity 75.2%; Pred. No. 0;
Matches 2364; Conservative 0; Mismatches 637; Indels 141; Gaps 14;

```

Qy      50 AACGCAGCGGCATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGC 109
        ||| |||      ||      |  |||| |  ||||| |||  ||||| |||||
Db      4  AACCAGAAAAGTGCCTGTTTCCTCAGAACCATCTGGTGACCATCTCAGGCTGACCATGGC 63

Qy     110 CCTCCCAGCCCTGGGCTGGACCCCTGGAGCCTCCTGGGCCCTTTTCCTCTTCCAAC TGCT 169
        ||| ||| ||||| ||||| |||| | ||||| ||||| |  |||  ||||| ||||| |
Db     64  CCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTCTTTTCTTCCAAC TCT 123

Qy     170 TCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCAGGGT 229
        |  |||||      | | | | | | | |||  ||  ||  ||||| ||||| ||||| ||
Db    124  CCTGCTGCCATCAC TGCCACCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCCAGAGT 183

Qy     230 CAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCA 289
        || |||| |||| || | | | | |||| || ||||| ||||| || | |||||
Db    184  CAAATACCATGCTGGAGACGGGCACAGGGCCCTCAGCTTCTTCCAACAAAAGGCCTCCG 243

Qy     290 GGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGA 349
        ||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    244  AGACTTTTGACACGCTGCTCCTGAGTGACGATGGCAACACTCTCTATGTGGGGGCTCGAGA 303

Qy     350 AGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACC 409
        ||| |  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    304  GGCCGTCCTGGCCTTGAATATCCAGAACCCAGGAATCCCAAGGCTAAAGAACATGATACC 363

Qy     410 GTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGAC 469

```

Db	364	 CTGGCCAGCCAGTGAGAGAAAAAAGACCGAATGTGCCTTTAAGAAGAAGAGCAATGAGAC	423
Qy	470	ACAGTGTTTCAACTTCATCCGTGTCTGGTTTCTTACAATGTCACCCATCTCTACACCTG	529
Db	424	 ACAGTGTTTCAACTTCATTCGAGTCCTGGTCTCTTACAATGCTACTCACCTCTATGCCCTG	483
Qy	530	CGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATT-----	566
Db	484	 TGGGACCTTTGCCTTCAGCCCTGCCTGTACCTTCATTACGTGCGACCCTGGCATTCTGGG	543
Qy	567	-----GAACTTCAAGATTCTTACCTGTTGCCCATCTCGGAG	602
Db	544	 CTCCCAGCCTCTTCCCCCTCTAGGAACTCCAAGATTCCCTCCTGTTGCCCATCTTGATA	603
Qy	603	GACAAGGTCATGGAGGGAAAAGGCCAAAGCCCTTTGACCCGCTCACAAGCATACGGCT	662
Db	604	 GACAAGGTCATGGACGGGAAGGCCAAAGCCCTTTGACCCTGTTCAACAAGCACACAGCT	663
Qy	663	GTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTTCCTGGGCAGTGAGCCC	722
Db	664	 GTCTTGGTCGATGGGATGCTTTATTCCGGCACCATGAACAACCTTCCTGGGCAGCGAGCCC	723
Qy	723	ATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACCTTCCTCCGCTGG	782
Db	724	 ATCCTGATGCGGACACTGGGATCCCAGCCTGTTCTCAAGACTGACATCTTCTTACGCTGG	783
Qy	783	CTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTC	842
Db	784	 CTGCACGCGGATGCCTCCTTCGTGGCAGCCATTCCATCCACCCAGGTCGTCTATTTCTTC	843
Qy	843	TTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGTGGCT	902
Db	844	 TTTGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAAGAGCTGTATATATCCAGGTGGCT	903
Qy	903	AGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTC	962
Db	904	 CAAGTCTGCAAGAACGACGTGGGCGGTGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTC	963
Qy	963	CTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCAC	1022
Db	964	 CTCAAAGCCCAGTTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCCGCCAC	1023
Qy	1023	GCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCC	1082
Db	1024	 GCGGTCCTGCTGCCCGCCGATTCTCCCTCTGTTTCCCGCATCTACGCAGTCTTTACCTCC	1083
Qy	1083	CAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGACATT	1142
Db	1084	 CAGTGGCAGGTTGGCGGGACCAGGAGCTCAGCAGTCTGTGCCTTCTCTCTCACGGACATT	1143
Qy	1143	GAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACT	1202
Db	1144	 GAGCGAGTCTTTAAAGGGAAGTACAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACT	1203
Qy	1203	TATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGGCCCTCCTCTGAT	1262

Db	1204	TACCGGGGCTCAGAGGTCAGCCCCAGGCCAGGCAGTTGCTCCATGGGCCCCCTCCTCTGAC	1263
Qy	1263	AAGGCCCTGACCTTCATGAAGGACCATTTCTCTGATGGATGAGCAAGTGGTGGGGACGCCC	1322
Db	1264	AAAGCCTTGACCTTCATGAAGGACCATTTTCTGATGGATGAGCACGTGGTAGGAACACCC	1323
Qy	1323	CTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCACTGGAGACAGCCCAGGGCCTT	1382
Db	1324	CTGCTGGTGAACTCTGGTGTGGAGTACACACGGCTTGCTGTGGAGTCAGCTCGGGGCCCTT	1383
Qy	1383	GATGGGCACAGCCATCTTGTCTGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCT	1442
Db	1384	GATGGGAGCAGCCATGTGGTCTGTATCTGGGTACCTCCACGGGGTCCCTGCACAAGGCT	1443
Qy	1443	GTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAGAGATTGAGCTGTTCCCTGACCTT	1502
Db	1444	GTGGTGCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATTGAGCTGAGCCCTGACTCT	1503
Qy	1503	GAACCTGTTTCGCAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTCA	1562
Db	1504	GAGCCTGTTTCGAAACCTGCAGCTGGCCCCCGCCAGGGTGCAGTGTTTGCAGGCTTCTCT	1563
Qy	1563	GGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGT	1622
Db	1564	GGAGGCATCTGGAGAGTTCAGGGCCAAATTGCACTGTCTACGAGAGCTGTGTGGACTGT	1623
Qy	1623	GTCCTTGCCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTG	1682
Db	1624	GTGCTGCNCAGGGACCCCTCACTGTGCCTGGGACCCTGAATCAAGACTCTGCAGCCTTCTG	1683
Qy	1683	TCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCA	1742
Db	1684	TCTGGCTCTACC---AAGCCTTGGAAAGCAGGACATGGAACGCGGCAACCCGGAGTGGGTA	1740
Qy	1743	TGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAATA	1802
Db	1741	TGCACCCGTGGCCCCATGGCCAGGAGCCCCGGCGTCAGAGCCCCCTCAACTAATTAATA	1800
Qy	1803	GAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCTTG	1862
Db	1801	GAAGTCCTGACAGTCCCCAACTCCATCCTGGAGCTGCCCTGCCCCACCTGTCAGCACTG	1860
Qy	1863	GCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTAC	1922
Db	1861	GCCTCTTACCACTGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGCTACCGTCTAC	1920
Qy	1923	AATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCA	1982
Db	1921	AATGGCTCCCTCTTGCTGCTGCCGAGGATGGTGTGCGGGGCCCTCTACCAGTGCTGGCG	1980
Qy	1983	ACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACC	2042
Db	1981	ACTGAGAACGGCTACTCATACCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCAGCCC	2040
Qy	2043	CTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACC	2102
Db	2041	CTGGCGCTGGACCTGAGCTGGCGGGCGTTCCCCGTGAGCGTGTGCAGGTCCCGCTGACC	2100

Qy 2103 AGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCTACTGGCCCCACTTTGTCACT 2162
 ||||| | || || || || ||||| ||||| ||||| ||||| |||||
 Db 2101 AGGGTCGGAGGCGGAGCTTCCATGGCTGCCAGCGGTCCCTACTGGCCCCATTTTCTCATC 2160

Qy 2163 GTCAGTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCA 2222
 || || ||||| | ||| | ||||| ||||| ||||| ||||| |||||
 Db 2161 GTTACCGTCCTCCTGGCCATCGTGCTCCTGGGAGTGCTCACTCTCCTCCTCGCTTCCCCA 2220

Qy 2223 TTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCGTGCGCCCTGGGGAG 2282
 || | || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2221 CTGGGGGCGCTGCGGGCTCGGGGTAAGGTTTCAGGGCTGTGGGATGCTGCCCCCAGGGAA 2280

Qy 2283 AAGGCCCCGTAAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCC 2342
 ||||| || | ||||| || || ||||| ||||| ||||| ||||| |||||
 Db 2281 AAGGCTCCACTGAGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCC 2340

Qy 2343 AGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACA 2402
 ||||| || || || ||||| ||||| || ||| | || |||||
 Db 2341 AGTGACGTAGATGCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACAGGGACACAG 2400

Qy 2403 GGCCGGGGCT--GCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
 ||| ||| || | ||| || ||||| || ||||| ||
 Db 2401 ATCCGCAGCTGAGCAGAGCAAGCCACTGGCCCTGTTGGCTATGC----- 2444

Qy 2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
 ||| | | | ||| |||||
 Db 2445 -----CAGGCACAGTGCCACTCTGACCAGGGTAGGAGGCTCTCCTGCTAA 2489

Qy 2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
 || |||| | ||| ||| ||| ||||| |||||
 Db 2490 CGTGTGTACCTACAGCACCCAGTAGGT-----CCTCCCCTGTGGGAC 2532

Qy 2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCAGACCTGCTCC 2640
 || ||||| | | || ||| ||| ||||| |||||
 Db 2533 TCTCTTCTGCAAGCACATTGGGCTGTCT-----CCATACCTGTACT 2573

Qy 2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
 | ||| | | | | | ||| ||| ||| ||| |||||
 Db 2574 TGTGCTGTGACAGGAAGAGCCAGACAGGTTCTTTGATTTTGATTGACCCAAGAGCCCTC 2633

Qy 2701 CAGAAACACAGTGTTCAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCATATGGTAA 2760
 | | |||| | || || || || || || || || || || || || ||
 Db 2634 CTGTAACAAACGTGCTCCAGGAGACCATGAAAGGTGTGGCTGTCTGGGATTCTGTGGTGA 2693

Qy 2761 TGAACACCAAACATCTAAACAATCATATGCTA-----ACATGCCACTCCTGGAAACTC 2813
 ||| | || |||| | ||| | |||| | | ||| |
 Db 2694 CAAAC-CTAAGCATCCGAGCAAGCTGGGGCTATTCCCTGCAAACCTCCATCCTGAACGCTGT 2752

Qy 2814 CACTCT----GAAGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAG 2868
 ||||| | ||||| ||||| ||||| || ||||| ||||| |||||
 Db 2753 CACTCTAGAAGCAGCTGCTGCTTTGAACACCAGCCACCTCCTTCCCAAGAGTCTCTAT 2812

Qy 2869 GGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTT 2928
 ||| || |||| || |||| ||||| ||||| ||| ||| | ||||| |
 Db 2813 GGAGTTGGCCCCCTTGTGTTTCCCTTTACCAGTCATGCCATACTGTTT---GGGAAGTCATC 2869

Query Match 43.7%; Score 1372.2; DB 9; Length 2172;
Best Local Similarity 71.9%; Pred. No. 0;
Matches 1560; Conservative 0; Mismatches 611; Indels 0; Gaps 0;

Qy	105	ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA	164
Db	1	ATGGCCCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTCCTCTTCCAA	60
Qy	165	CTGCTTCAGCTGCTGCTGCCGACGACGACCGGGGGAGGCGGGCAGGGGCCCATGCC	224
Db	61	CTCTTCCTGCTGCCATCACTGCCACCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCC	120
Qy	225	AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCCTTAGCTTCTTCCACCAGAAGGGC	284
Db	121	AGAGTCAAATACCATGCTGGAGACGGGCACAGGGCCCTCAGCTTCTTCCAACAAAAAGGC	180
Qy	285	CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT	344
Db	181	CTCCGAGACTTTGACACGCTGCTCCTGAGTGACGATGGCAACACTCTCTATGTGGGGGCT	240
Qy	345	CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATG	404
Db	241	CGAGAGGCCGTCTTGGCCTTGAATATCCAGAACCAGGAATCCCAAGGCTAAAGAACATG	300
Qy	405	ATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT	464
Db	301	ATACCTTGGCCAGCCAGTGAGAGAAAAAGACCGAATGTGCCTTTAAGAAGAAGAGCAAT	360
Qy	465	GAGACACAGTGTTTCAACTTCATCCGTGTCTTGGTTTCTTACAATGTCACCCATCTCTAC	524
Db	361	GAGACACAGTGTTTCAACTTCATTCGAGTCCTGGTCTCTTACAATGCTACTCACCTCTAT	420
Qy	525	ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTAC	584
Db	421	GCCTGTGGGACCTTTGCCTTCAGCCCTGCCTGTACCTTCATTGAACTCCAAGATTCCTTC	480
Qy	585	CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC	644
Db	481	CTGTTGCCCATCTTGATAGACAAGGTCATGGACGGGAAGGGCCAAAGCCCCTTTGACCCCT	540
Qy	645	GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC	704
Db	541	GTTCACAAGCACACAGCTGTCTTGGTCGATGGGATGCTTTATTCCGGCACCATGAACAAC	600
Qy	705	TTCTTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCAAGACC	764
Db	601	TTCTTGGGCAGCGAGCCCATCCTGATGCGGACACTGGGATCCCAGCCTGTCTCAAGACT	660
Qy	765	GACAACTTCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC	824
Db	661	GACATCTTCTTACGCTGGCTGCACGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	720
Qy	825	CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC	884
Db	721	NN	780
Qy	885	CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGGCAAAGCTGCTGCAG	944

[illegible]

Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
907.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CS0AL002BH02NP1&c=907.f>.


```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1064)
AUTHORS        Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE          Full-length cDNA libraries and normalization
JOURNAL        Unpublished (2001)
COMMENT        On May 5, 2003 this sequence version replaced gi:30384744.
                Contact: Genoscope
                Genoscope - Centre National de Sequencage
                2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
                Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
                end enriched, double-strand cDNA was digested with Not I and cloned
                into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
                was normalized. Library was constructed by Life Technologies, a
                division of Invitrogen. This sequence belongs to sequence cluster
                907.f
                For more information about this cluster, see
                http://www.genoscope.cns.fr/cdna?s=CS0DL005AB09NP1&c=907.f.
FEATURES
  source        Location/Qualifiers
                1. .1064
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CS0DL005YC17"
                /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                /cell_line="RAMOS CELL LINE"
                /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                25-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo(dT)
                primer. Five prime end enriched, double-strand cDNA was
                digested with Not I and cloned into the Not I and EcoR V
                sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match      29.5%;   Score 926.2;   DB 5;   Length 1064;
Best Local Similarity 95.5%;   Pred. No. 1.2e-233;
Matches 1000;   Conservative 15;   Mismatches 24;   Indels 8;   Gaps 6;

Qy      2058  GAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGG 2117
          || |||  |||| |  || | | : |:||||||||||| :|||||||||||
Db      1040  GATCTGAATGGCAGCATCCCCCGGGAGMWGKGARGTCCCGTTGACC-RGGTCAGTGGTGGG 982

Qy      2118  GCCGCCCTGGCTGCCCAGCAGTCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTT 2177
          |  ||  | :|||||||||||:|:|  ||  |||||||||||||||||||
Db      981  --CCGCCCTGGYGCCAGCAGTCCWAYTG--CCCCATTTGTCACTGTCACTGTCTCTTT 926

Qy      2178  GCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGG 2237
          ||||||||||||| ||||||||||||| |||||||||||||||||||
Db      925  GCCTTAGTGCTTTCA-GAGCCCTCATCATCCTCGT-GCCTCCCCATTGAGAGCACTCCGG 868

Qy      2238  GCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGC 2297
          ||||||||||||| ||||||||||||| |||||||||||||||||||
Db      867  GCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGC 808

Qy      2298  AGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCT 2357
          ||||||||||||| ||||||||||||| |||||||||||||||||||

```

Db	807	AGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCT	748
Qy	2358	GACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT	2417
Db	747	GACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT	688
Qy	2418	GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA	2477
Db	687	GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA	628
Qy	2478	GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC	2537
Db	627	GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC	568
Qy	2538	ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC	2597
Db	567	ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC	508
Qy	2598	ATGAGCTCTCTAACAGGGTGGGGGTACCCCCAGACCTGCTCCTACACTGATATTGAAGA	2657
Db	507	ATGAGCTCTCTAACAGGGTGGGGGTACCCCCAGACCTGCTCCTACACTGATATTGAAGA	448
Qy	2658	ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC	2717
Db	447	ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC	388
Qy	2718	AAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTA	2777
Db	387	AAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTA	328
Qy	2778	AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC	2837
Db	327	AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC	268
Qy	2838	ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA	2897
Db	267	ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA	208
Qy	2898	GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCT	2957
		: :	
Db	207	GTCGTGCACCGCTGACTYCCAGGAAGTCTTCCCTGAAKTCTGACCACCTTTCTTCTTGCT	148
Qy	2958	TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG-CAGGGGTAATCTGAGC	3016
		: : :	
Db	147	TCAGTTGGGGCAGAYTYTGATCCCTTCTGCCCTGGYAGAATGGTCAGGGGTAATCTGAGC	88
Qy	3017	CTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTT	3076
		: : :	
Db	87	CTTCTTCACTCCTTTACCCTAGCTGACCCCTTCMCCTCTCCCBTSSCTTTTCCTTTGTT	28
Qy	3077	TTGGGATTCAGAAAACCTGCTTGTGAGA	3103
Db	27	TTGGGATTCAGAAAACCTGCTTGTGAGA	1

LOCUS BX350606 922 bp mRNA linear EST 08-APR-2004
DEFINITION BX350606 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL005YC17 3-PRIME, mRNA sequence.

ACCESSION BX350606

VERSION BX350606.1 GI:30373499

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 922)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
907.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0BAI043ZD06_CS04076_1&c=907.f.

FEATURES Location/Qualifiers

source

1. .922

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DL005YC17"

/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"

/cell_line="RAMOS CELL LINE"

/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 27.8%; Score 874.4; DB 5; Length 922;

Best Local Similarity 98.7%; Pred. No. 6.1e-220;

Matches 878; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1372 CCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGC 1431
||||| ||||||||||||||||||||||||||||||| ||||||| |||||||

Db 919 CCCAGGNCCTTGATGGGCACAGCCATCTTGTCATGTACTTGGGAACCACAACAGGGTCGC 860

Qy 1432 TCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGGAAGAGATTCAGCTGT 1491
||||| ||||||||||||||||||||||||||||||| ||||||| |||||||

Db 859 TCCACAAGACTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGGAAGAGATTCAGCTGT 800

Qy 1492 TCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTTG 1551
||||| ||||||||||||||||||||||||||||||| ||||| |||||||

Db 799 TCCCTGACCCTGANCTGTTTCGCAACCTGCAGCTGGCCNCCACCAAGGGTGCAGTGTTGN 740

Qy	1552	TAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCT	1611
Db	739	TAGGCTTCTCAGNAGGTGTCTGGAGGGTGCNCCGAGCCAACTGTAGTGTCTATGAGAGCT	680
Qy	1612	GTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCCTGGGACCCTGAGTCCCGAACCT	1671
Db	679	GTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCCTGGGACCCTGAGTCCCGAACCT	620
Qy	1672	GTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACC	1731
Db	619	GTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACC	560
Qy	1732	CAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGC	1791
Db	559	CAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGC	500
Qy	1792	AAATCATTAAGAAGTCCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACC	1851
Db	499	AAATCATTAAGAAGTCCCTGGCTGTCCCTAACTCCATCCTGGAGCTCCCCTGCCCCACC	440
Qy	1852	TGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTT	1911
Db	439	TGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTT	380
Qy	1912	CCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACC	1971
Db	379	CCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACC	320
Qy	1972	AGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCC	2031
Db	319	AGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCC	260
Qy	2032	AGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGG	2091
Db	259	AGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGG	200
Qy	2092	TCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCCTACTGGCCCC	2151
Db	199	TCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCCTACTGGCCCC	140
Qy	2152	ACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCG	2211
Db	139	ACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCG	80
Qy	2212	TGGCCTCCCCATTGAGAGCACTCCGGGGCTCGGGGCAAGGTTTCAGGGCTGT	2261
Db	79	TGGCCTCCCCATTGAGAGCACTCCGGGGCTCGGGGCAAGGTTTCAGGGCTGT	30

RESULT 11

BX384966

LOCUS BX384966 934 bp mRNA linear EST 23-APR-2004

DEFINITION BX384966 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL005YC17 5-PRIME, mRNA sequence.

ACCESSION BX384966

VERSION BX384966.2 GI:46556002

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 934)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 8, 2003 this sequence version replaced gi:30436505.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
907.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CS0DL005AB09QP1&c=907.f>.

FEATURES Location/Qualifiers

source 1. .934
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL005YC17"
/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 27.0%; Score 849.2; DB 5; Length 934;
Best Local Similarity 97.0%; Pred. No. 2.9e-213;
Matches 871; Conservative 4; Mismatches 22; Indels 1; Gaps 1;

Qy 99 CTGAGCATGGCCCTCCCAGCCCTGGGCGCTGGACCCCTGGAGCCTCCTGGGCGCTTTTCCTC 158
|||||

Db 1 CTGAGCATGGCCCTCCCAGCCCTGGGCGCTGGACCCCTGGAGCCTCCTGGGCGCTTTTCCTC 60

Qy 159 TTCCAAC TGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCC 218
|||||

Db 61 TTCCAAC TGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCC 120

Qy 219 ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG 278
|||||

Db 121 ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG 180

Qy 279 AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG 338
|||||

Db 181 AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG 240

Qy	339	GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAG	398
Db	241	GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAG	300
Qy	399	AACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAG	458
Db	301	AACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAG	360
Qy	459	AGCAATGAGACACAGTGTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCAT	518
Db	361	AGCAATGAGACACAGTGTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCAT	420
Qy	519	CTCTACACCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGACCTTCATTGAACTTCAAGAT	578
Db	421	CTCTACACCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGACCTTCATTGAACTTCAAGAT	480
Qy	579	TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT	638
Db	481	TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT	540
Qy	639	GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG	698
Db	541	GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG	600
Qy	699	AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC	758
Db	601	AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC	660
Qy	759	AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT	818
Db	661	AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT	720
Qy	819	TCGACCCAGTCTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG	878
Db	721	TCGACCCAGTCTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG	780
Qy	879	AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG	938
Db	781	AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCG-AAARCTG	839
Qy	939	CTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGC	996
Db	840	CTGCAGAAGAAGTGGACCMCCTCCTGAAGCCCACYGCTCMCCAGCCGGGCACTGC	897

RESULT 12

BX328255

LOCUS BX328255 897 bp mRNA linear EST 07-APR-2004

DEFINITION BX328255 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED

Homo sapiens cDNA clone CS0DL005YC17 5-PRIME, mRNA sequence.

ACCESSION BX328255

VERSION BX328255.2 GI:46262160

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 897)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 1, 2003 this sequence version replaced gi:30307730.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 907.f
 For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAG053ZH06_CS05040_1&c=907.f.

FEATURES Location/Qualifiers

source 1. .897
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DL005YC17"
 /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
 /cell_line="RAMOS CELL LINE"
 /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 26.7%; Score 839; DB 5; Length 897;
 Best Local Similarity 99.0%; Pred. No. 1.5e-210;
 Matches 886; Conservative 0; Mismatches 5; Indels 4; Gaps 4;

Qy	805	TGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGG-AGACAGCCAGCGAG	863
Db	1	TGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAAGACAGCCAGCGAG	60
Qy	864	TTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTG	923
Db	61	TTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTG	120
Qy	924	GGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGC	983
Db	121	GGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGC	180
Qy	984	ACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGAT	1043
Db	181	ACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGAT	240
Qy	1044	TCTCCACAGCTCCCCACATCTACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGACC	1103
Db	241	TCTCCACAGCTCCCCACATCTACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGACC	300

Qy	1104	AGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAA	1163
Db	301	AGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAA	360
Qy	1164	TACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAAC	1223
Db	361	TACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAAC	420
Qy	1224	CCCCGGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAG	1283
Db	421	CCCCGGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAG	480
Qy	1284	GACCATTTCTTGATGGATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTG	1343
Db	481	GACCATTTCTTGATGGATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTG	540
Qy	1344	GAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTC	1403
Db	541	GAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTC	600
Qy	1404	ATGTACCTGGGAACCAACACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT	1463
Db	601	ATGTACCTGGGAACCAACACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT	660
Qy	1464	GCTCATCTGGTGAAGAGATTTCAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAG	1523
Db	661	GCTCATCTGGTGAAGAGATTTCAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAG	720
Qy	1524	CTGGCCCCCACCAGGGTGCA-GTGTGTTGTAGGCTTCTCAGGAGGTGTCTGG-AGGGTGC	1581
Db	721	CTGGCCCCCACCAGGGTGCA-GTGTGTTGTAGGCTTCTCAGGAGGTGTCTGGNAGGGTGC	780
Qy	1582	CCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCCGGACCCCC	1641
Db	781	CCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCCGGACCCCC	840
Qy	1642	ACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCT	1696
Db	841	-CTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCT	894

RESULT 13

BQ057192

LOCUS BQ057192 974 bp mRNA linear EST 29-MAR-2002

DEFINITION AGENCOURT_6769628 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5812383 5', mRNA sequence.

ACCESSION BQ057192

VERSION BQ057192.1 GI:19816532

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 974)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2062 row: 1 column: 16
High quality sequence stop: 714.

FEATURES Location/Qualifiers
source 1. .974
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5812383"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 26.3%; Score 827.4; DB 5; Length 974;
Best Local Similarity 92.6%; Pred. No. 1.8e-207;
Matches 902; Conservative 0; Mismatches 67; Indels 5; Gaps 3;

Qy	92	TCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCCTGGACCCCTGGAGCCTCCTGGGCCT	151
Db	1	TCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCCTGGACCCCTGGAGCCTCCTGGGCCT	60
Qy	152	TTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCA	211
Db	61	TTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCA	120
Qy	212	GGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTT	271
Db	121	GGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTT	180
Qy	272	CCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCT	331
Db	181	CCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCT	240
Qy	332	CTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAG	391
Db	241	CTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAG	300
Qy	392	GCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAA	451

```

      |||
Db      301 GCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAA 360
Qy      452 GAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGTCCTGGTTTCTTACAATGT 511
      |||
Db      361 GAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGTCCTGGTTTCTTACAATGT 420
Qy      512 CACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACT 571
      |||
Db      421 CACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACT 480
Qy      572 TCAAGATTCTTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAG 631
      |||
Db      481 TCAAGATTCTTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAG 540
Qy      632 CCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGG 691
      |||
Db      541 CCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGG 600
Qy      692 TACTATGAACAACTTCCTGGGCAGTGAGCCCATCTGATGCGCACACTGGGATCCCAGCC 751
      |||
Db      601 TACTATGAACAACTTCCTGGGCAGTGAGCCCATCTGATGCGCACACTGGGATCCCAGCC 660
Qy      752 TGTCCCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGC 811
      |||
Db      661 TGTCCCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGC 720
Qy      812 CATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTT 871
      |||
Db      721 CATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTT 780
Qy      872 CTTTGAGAGGCTCCACACATCGCGGGTGG-CTAGAGTCTGCAAGAATGACGTGGGC-GGC 929
      |||
Db      781 CTTTGAGAGGCCCCACCCTCCCGGGGGCCCTANAGTCTGCCAAAATGACGTGGGCGGGC 840
Qy      930 GAAAAGCTGCTGCAGAAGAA---GTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACC 986
      |||
Db      841 GAAAAGCTGCTGCAAAAAAAGTGGACCCCTTCCTTGAAGGCCAGCTGCTCTGGCCC 900
Qy      987 CAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCT 1046
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      901 CCAGCCGGGGGAGCTTGCCCTTTCACGTCATTCCCGCCCCGGGGTCTGGCTCCCCC 960
Qy      1047 CCCACAGCTCCCCA 1060
      || | | | |
Db      961 CCGAATTTTCCCCA 974

```

RESULT 14

BX390196

LOCUS BX390196 944 bp mRNA linear EST 29-APR-2004

DEFINITION BX390196 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
cDNA clone CS0DD003YE08 5-PRIME, mRNA sequence.

ACCESSION BX390196

VERSION BX390196.2 GI:46873199

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 944)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 8, 2003 this sequence version replaced gi:30463276.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
907.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAG009ZD12_CS00860_1&c=907.f.

FEATURES
source Location/Qualifiers
1. .944
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD003YE08"
/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 26.1%; Score 820.4; DB 5; Length 944;
Best Local Similarity 97.4%; Pred. No. 1.3e-205;
Matches 897; Conservative 0; Mismatches 17; Indels 7; Gaps 6;

Qy 1535 CCAGGGTGCAGTGT TTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTG 1594
|||||

Db 1 CCAGGGTGCAGTGT TTTGTAGGCTTCT-AGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTG 59

Qy 1595 TAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGA 1654
|||||

Db 60 TAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGA 119

Qy 1655 CCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGA 1714
|||||

Db 120 CCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGA 179

Qy 1715 CATGGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCG 1774
|||||

Db 180 CATGGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCG 239

Qy 1775 GCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGA 1834
|||||

Db 240 GCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGA 299

Qy	1835	GCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGC	1894
Db	300	GCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGC	359
Qy	1895	AGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGG	1954
Db	360	AGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGG	419
Qy	1955	AGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTC	2014
Db	420	AGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTC	479
Qy	2015	CTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCC	2074
Db	480	CTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCC	539
Qy	2075	CCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCA	2134
Db	540	CCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCA	599
Qy	2135	GCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCCTCTTGCCTTAGTGCTTTCAGG	2194
Db	600	GCAGTCCTACTGGCCCCACTTGTCACTGTCACTGTCCCTCTTGCCTTAGTGCTTTCAGG	659
Qy	2195	AGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTC-	2253
Db	660	AGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTTCGGGCAAGGTTCA	719
Qy	2254	AGGGCTGTGAGACCCTGCGCCCTGGGG--AGAAGGCCCGTTAAGCAGAGAGCAACA-CC	2310
Db	720	AGGGCTGTGAGACCCTGCGCCCTGGGGGAGAAAGGCCCGTTAAGCAGAGAGCAACACCC	779
Qy	2311	TCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACG-CTGACAACAACCTGC	2369
Db	780	TTCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGGCGCCTGACAACAACCTGC	839
Qy	2370	CTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGG	2429
Db	840	CTAGGCACTGAGGTAGCTTAAACTCTA-GCACAGCCGGGGCTTGCGGGGCAGCCACCTGC	898
Qy	2430	CCATGCTGGCTGGGCGGCCCA	2450
Db	899	CCATGCTGTGTGGGCGGCCCA	919

RESULT 15
CB243787/c

LOCUS	CB243787	797 bp	mRNA	linear	EST 12-FEB-2003
DEFINITION	UI-CF-FN0-agg-a-05-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone UI-CF-FN0-agg-a-05-0-UI 3', mRNA sequence.				
ACCESSION	CB243787				
VERSION	CB243787.1 GI:28365431				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 797)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA sequence: 1-46, >AT-rich#Low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source Location/Qualifiers

1. .797

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-CF-FN0-agg-a-05-0-UI"

/tissue_type="Human Lung Epithelial cells"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-CF-FN0"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-FN0 is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu

TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h

TAG_LIB=UI-CF-FN0

TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 24.8%; Score 779.8; DB 6; Length 797;

Best Local Similarity 99.4%; Pred. No. 7e-195;

Matches 781; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2358 GACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT 2417

|||||

Db 797 GACAACAACCTGCNTAGGCACTGAGGTAGCTTAAACTNTAGGCACAGGCCGGGGCTGCGGT 738

Qy	2418	GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA	2477
Db	737	GCAGGCACCCGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGANTAGGATGACAGCA	678
Qy	2478	GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC	2537
Db	677	GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC	618
Qy	2538	ACTCAGCAGGGTGATGCACAGCAGTCTGCCCTCCCCTATGGGACTCCCTTCTACCAAGCAC	2597
Db	617	ACTCAGCAGGGTGATGCACAGCAGTCTGCCCTCCCCTATGGGACTCCCTTCTACCAAGCAC	558
Qy	2598	ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA	2657
Db	557	ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA	498
Qy	2658	ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCCTCCAGAAACACAGTGTTTC	2717
Db	497	ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCCTCCAGAAACACAGTGTTTC	438
Qy	2718	AAGAGACCCCTAAAAAACCTGCCTGTCCCAGGACCCCTATGGTAATGAACACCAAACATCTA	2777
Db	437	AAGAGACCCCTAAAAAACCTGCCTGTCCTAGGACCCCTATGGTAATGAACACCAAACATCTA	378
Qy	2778	AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC	2837
Db	377	AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC	318
Qy	2838	ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA	2897
Db	317	ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA	258
Qy	2898	GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCT	2957
Db	257	GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCT	198
Qy	2958	TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCC	3017
Db	197	TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCC	138
Qy	3018	TTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCCTTTGTTT	3077
Db	137	TTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCCTTTGTTT	78
Qy	3078	TGGGATTTCAGAAAACCTGCTTGTCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTA	3137
Db	77	TGGGATTTCAGAAAACCTGCTTGTCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTA	18
Qy	3138	AAAAAA 3143	
Db	17	AAAAAA 12	

Search completed: February 15, 2005, 13:17:35
Job time : 9877 secs

OM nucleic - nucleic search, using sw model

Run on: February 14, 2005, 22:56:12 ; Search time 9798 Seconds
 (without alignments)
 12210.247 Million cell updates/sec

Title: US-10-015-391A-276
 Perfect score: 3143
 Sequence: 1 gggctgaggcactgagagac.....aaatataaggcttaaaaaaa 3143

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est2:*
 3: gb_htc:*
 4: gb_est3:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_gss1:*
 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3005	95.6	3005	3	CR623694	CR623694 full-leng
2	2927.6	93.1	3151	3	HSM807023	BX640891 Homo sapi
3	1874	59.6	2172	9	AY402621	AY402621 Homo sapi
4	1765.4	56.2	2133	9	AY402622	AY402622 Pan trogl
5	1747.4	55.6	3206	3	AK077976	AK077976 Mus muscu
6	1701.4	54.1	3086	3	AK035918	AK035918 Mus muscu
7	1372.2	43.7	2172	9	AY402623	AY402623 Mus muscu
c 8	950.6	30.2	1108	5	BX367242	BX367242 BX367242

c	9	926.2	29.5	1064	5	BX363741	BX363741	BX363741
c	10	874.4	27.8	922	5	BX350606	BX350606	BX350606
	11	849.2	27.0	934	5	BX384966	BX384966	BX384966
	12	839	26.7	897	5	BX328255	BX328255	BX328255
	13	827.4	26.3	974	5	BQ057192	BQ057192	AGENCOURT
	14	820.4	26.1	944	5	BX390196	BX390196	BX390196
c	15	779.8	24.8	797	6	CB243787	CB243787	UI-CF-FN0
	16	775	24.7	801	5	BX112994	BX112994	BX112994
	17	769.8	24.5	912	5	BQ883972	BQ883972	AGENCOURT
	18	768	24.4	958	5	BX376660	BX376660	BX376660
	19	757.6	24.1	892	6	CD107028	CD107028	AGENCOURT
c	20	756.2	24.1	819	6	CD631371	CD631371	56050427H
	21	748.6	23.8	951	5	BQ056228	BQ056228	AGENCOURT
	22	696.6	22.2	775	1	AU122156	AU122156	AU122156
	23	691.2	22.0	970	5	BQ707628	BQ707628	AGENCOURT
	24	681	21.7	1066	4	BM806752	BM806752	AGENCOURT
c	25	675.2	21.5	763	6	CD631373	CD631373	56066030H
	26	674	21.4	727	7	CN255817	CN255817	170004252
	27	673	21.4	960	5	BX367243	BX367243	BX367243
	28	666	21.2	706	6	CD631372	CD631372	56050427J
	29	664	21.1	681	7	CV023527	CV023527	490 Full
	30	661.8	21.1	666	4	BG684636	BG684636	602635914
	31	650	20.7	925	5	BQ937439	BQ937439	AGENCOURT
c	32	627.4	20.0	640	6	CA311774	CA311774	UI-CF-FN0
c	33	612	19.5	624	4	BM666780	BM666780	UI-E-CL1-
	34	609.8	19.4	1119	4	BI550650	BI550650	603195823
	35	608.4	19.4	803	7	CN539797	CN539797	UI-M-HU0-
	36	598.6	19.0	621	2	AW965845	AW965845	EST377918
c	37	598.4	19.0	634	5	BU632880	BU632880	UI-H-FE1-
c	38	594	18.9	618	5	BU686374	BU686374	UI-CF-DU1
	39	590.8	18.8	740	6	CD631374	CD631374	56066030J
	40	585.2	18.6	881	5	BQ960065	BQ960065	AGENCOURT
	41	579.2	18.4	720	6	CA315771	CA315771	UI-M-FW0-
	42	579	18.4	580	5	BP346261	BP346261	BP346261
	43	576.2	18.3	582	5	BP312448	BP312448	BP312448
	44	568.6	18.1	783	7	CK483764	CK483764	AGENCOURT
	45	566.8	18.0	582	5	BP305311	BP305311	BP305311
	46	565.8	18.0	571	7	CR554650	CR554650	DKFZp4590
	47	557.8	17.7	796	5	BU052878	BU052878	UI-M-FC0-
	48	554.4	17.6	718	7	CK837783	CK837783	4063044 B
	49	552.6	17.6	917	6	CA454892	CA454892	AGENCOURT
	50	552.4	17.6	779	4	BI683727	BI683727	603306287
	51	551.4	17.5	695	4	BG685741	BG685741	602637838
	52	547	17.4	547	4	BM128651	BM128651	if14b09.y
	53	546.6	17.4	709	5	BQ573544	BQ573544	UI-M-FD0-
	54	542.6	17.3	667	4	BG703963	BG703963	602687061
	55	542.2	17.3	784	5	BQ043061	BQ043061	UI-M-EG0p
	56	538.6	17.1	841	6	CB566426	CB566426	AGENCOURT
	57	530	16.9	550	5	BP292524	BP292524	BP292524
	58	528	16.8	528	6	CA393520	CA393520	cs39b03.y
	59	526.2	16.7	944	4	BI250501	BI250501	602993551
	60	524.4	16.7	858	7	CK022938	CK022938	AGENCOURT
c	61	522.4	16.6	536	5	BQ356019	BQ356019	PM3-HT130
	62	510.8	16.3	793	4	BI146386	BI146386	602910749
	63	510	16.2	666	2	BE868099	BE868099	601443414
	64	507.8	16.2	519	7	CK819350	CK819350	if14b09.y
	65	500.2	15.9	532	4	BM691378	BM691378	UI-E-CI1-

	66	500.2	15.9	758	4	BI105301	BI105301	602893591
c	67	498	15.8	567	1	AU147813	AU147813	AU147813
	68	495.4	15.8	628	7	CN792080	CN792080	4126901 B
	69	494	15.7	598	2	BE588408	BE588408	194035 BA
	70	486.6	15.5	788	7	CK481778	CK481778	AGENCOURT
	71	486	15.5	969	4	BG247839	BG247839	602359548
	72	481.6	15.3	632	7	CK625364	CK625364	mi32c08.y
	73	481	15.3	481	4	BM694992	BM694992	UI-E-CL1-
c	74	478.8	15.2	503	1	AI817099	AI817099	wj76h11.x
	75	478.8	15.2	810	6	CB587284	CB587284	AGENCOURT
	76	476.8	15.2	544	4	BI481387	BI481387	H2RPE-174
	77	470.4	15.0	530	1	AA481246	AA481246	aa34h11.r
c	78	469.2	14.9	562	2	AW836429	AW836429	PM3-LT003
	79	467.8	14.9	821	5	BQ442696	BQ442696	UI-M-EV0-
	80	465.4	14.8	806	7	CK481746	CK481746	AGENCOURT
	81	464.6	14.8	585	4	BI359871	BI359871	384615 MA
	82	462.6	14.7	667	2	AW914963	AW914963	EST346267
	83	462.2	14.7	887	4	BI219079	BI219079	602938695
	84	461.4	14.7	672	6	BY747595	BY747595	BY747595
	85	461.2	14.7	892	5	BQ934892	BQ934892	AGENCOURT
	86	449.6	14.3	537	2	AW657913	AW657913	93554 MAR
	87	447	14.2	872	4	BI150290	BI150290	602915311
c	88	446.4	14.2	450	1	AI568200	AI568200	tn66h01.x
	89	444	14.1	822	7	CO565372	CO565372	AGENCOURT
	90	443.8	14.1	659	6	BY747925	BY747925	BY747925
c	91	443.4	14.1	456	5	BU726485	BU726485	UI-E-CI1-
c	92	442.4	14.1	444	5	BQ356020	BQ356020	PM3-HT130
c	93	440.6	14.0	468	5	BQ356018	BQ356018	PM3-HT130
	94	439.6	14.0	578	4	BI341318	BI341318	368709 MA
c	95	436.8	13.9	440	1	AA973640	AA973640	oo48c04.s
	96	435.2	13.8	579	4	BI360284	BI360284	387146 MA
	97	432.4	13.8	621	9	CG591258	CG591258	OST245642
	98	431	13.7	632	7	CO581119	CO581119	ILLUMIGEN
	99	430.8	13.7	794	2	BF578994	BF578994	602096109
	100	427	13.6	563	4	BM030859	BM030859	495387 MA
c	101	426.8	13.6	441	1	AA554541	AA554541	nl14b01.s
	102	426.8	13.6	827	7	CO404310	CO404310	AGENCOURT
	103	425.2	13.5	443	2	BF882612	BF882612	QV3-ET020
c	104	425.2	13.5	457	1	AI291110	AI291110	qml0d09.x
	105	422.8	13.5	546	2	BF199358	BF199358	249500 MA
	106	422.4	13.4	759	4	BG243769	BG243769	602357081
	107	418.4	13.3	576	4	BI345630	BI345630	374508 MA
c	108	415	13.2	415	1	AI017230	AI017230	ou32d12.x
	109	415	13.2	536	2	BF199378	BF199378	249524 MA
c	110	414.6	13.2	454	2	BF882611	BF882611	QV3-ET020
	111	414.6	13.2	538	2	BF080018	BF080018	230753 MA
c	112	413.6	13.2	537	5	BX372943	BX372943	BX372943
	113	413	13.1	583	5	BP315573	BP315573	BP315573
c	114	412.6	13.1	468	7	T34379	T34379	EST66750 Hu
	115	412	13.1	582	5	BP314196	BP314196	BP314196
	116	411	13.1	581	5	BP314893	BP314893	BP314893
	117	410.8	13.1	624	4	BM691301	BM691301	UI-E-CI1-
	118	409	13.0	582	5	BP312657	BP312657	BP312657
	119	409	13.0	721	2	BF580373	BF580373	602097124
	120	408	13.0	473	7	H08023	H08023	yl91d06.r1
	121	406	12.9	406	7	CR538178	CR538178	DKFZp459F
	122	405	12.9	583	5	BP314892	BP314892	BP314892

	123	404.8	12.9	870	2	BE306403	BE306403	601102295
	124	404.6	12.9	610	4	BG618720	BG618720	602645175
	125	403.2	12.8	1122	2	BF159534	BF159534	601769029
c	126	402.6	12.8	449	1	AI623385	AI623385	ts18g03.x
	127	401.4	12.8	581	5	BP357544	BP357544	BP357544
	128	395.4	12.6	634	1	AA646591	AA646591	ve46d08.r
	129	394.8	12.6	494	4	BM288077	BM288077	528964 MA
	130	392.4	12.5	766	7	CK478839	CK478839	AGENCOURT
	131	392.2	12.5	882	2	BE571537	BE571537	601333983
	132	392	12.5	582	5	BP315572	BP315572	BP315572
	133	391.6	12.5	555	6	CB613565	CB613565	AMGNNUC:N
	134	390.6	12.4	581	6	CB606887	CB606887	AMGNNUC:N
	135	388.8	12.4	465	2	BF882607	BF882607	QV3-ET020
	136	388	12.3	618	6	CB579294	CB579294	AMGNNUC:N
	137	387.4	12.3	544	4	BI961174	BI961174	MONO1_7_A
c	138	387	12.3	405	1	AI221749	AI221749	qg93f04.x
	139	383	12.2	713	6	BY763638	BY763638	BY763638
c	140	380.8	12.1	412	1	AA761091	AA761091	ny13g11.s
	141	378	12.0	598	1	AV617761	AV617761	AV617761
	142	377.4	12.0	535	5	BQ552175	BQ552175	H4013H07-
	143	377.2	12.0	665	4	BI151295	BI151295	602917272
c	144	374.4	11.9	459	2	BF154829	BF154829	PM2-BT076
c	145	374.4	11.9	459	4	BG949399	BG949399	PM2-BT076
	146	372.4	11.8	582	5	BP314933	BP314933	BP314933
	147	370.6	11.8	600	6	CA530364	CA530364	9034-81 M
	148	370.2	11.8	541	2	AW654459	AW654459	103930 MA
c	149	369.4	11.8	464	5	BQ356179	BQ356179	PM3-HT130
	150	367.4	11.7	490	2	AW659681	AW659681	97213 MAR
	151	367	11.7	516	2	BF075002	BF075002	223731 MA
c	152	366.4	11.7	369	2	AW593031	AW593031	hg07e10.x
	153	363.8	11.6	368	1	AA419534	AA419534	zv03c09.r
	154	363.4	11.6	513	4	BM106299	BM106299	509997 MA
	155	360.6	11.5	742	6	CB249229	CB249229	UI-M-FC0-
	156	356.4	11.3	583	5	BP357148	BP357148	BP357148
	157	355	11.3	529	5	BU698229	BU698229	LL2in1365
c	158	354.4	11.3	363	1	AI221756	AI221756	qg93f12.x
	159	353	11.2	576	4	BI914790	BI914790	603184176
c	160	351.4	11.2	737	7	CO425778	CO425778	UI-M-HU0-
	161	348	11.1	360	7	T19441	T19441	f03002s Tes
c	162	346	11.0	358	1	AI682007	AI682007	tp45g08.x
	163	344.8	11.0	502	5	BU696522	BU696522	LL2in1072
	164	344.2	11.0	623	2	BB628588	BB628588	BB628588
	165	343.6	10.9	424	2	AW352877	AW352877	35717 MAR
	166	340.4	10.8	552	2	AW655294	AW655294	106095 MA
	167	338.6	10.8	449	5	BQ336149	BQ336149	PM0-MT042
	168	337.2	10.7	545	2	AW654538	AW654538	104068 MA
	169	334.8	10.7	479	4	BM088355	BM088355	501805 MA
	170	333.2	10.6	411	2	BE859656	BE859656	UI-M-AL0-
	171	332.2	10.6	443	2	AW355069	AW355069	37338 MAR
	172	327.4	10.4	700	5	BM944176	BM944176	UI-M-EH0p
c	173	326.8	10.4	330	7	CK819349	CK819349	if14b09.x
	174	321.8	10.2	469	1	AJ650325	AJ650325	AJ650325
	175	321.2	10.2	445	2	AW481698	AW481698	37332 MAR
	176	320.6	10.2	433	2	AW355070	AW355070	37337 MAR
	177	318.6	10.1	390	6	CB778065	CB778065	AMGNNUC:C
	178	318.4	10.1	432	2	BF019645	BF019645	ux14b02.y
c	179	316.8	10.1	353	2	AW628784	AW628784	hi39e03.x

	180	316.2	10.1	465	7	R81743	R81743 yj05d01.r1
c	181	315.8	10.0	469	1	AI141990	AI141990 oo17g10.x
	182	312.4	9.9	443	4	BM106612	BM106612 510531 MA
c	183	310.6	9.9	346	5	BQ335891	BQ335891 PM3-MT020
c	184	310	9.9	356	2	AW298440	AW298440 UI-H-BW0-
c	185	308.4	9.8	310	1	AA687813	AA687813 nv12e08.s
c	186	308	9.8	456	7	CV374906	CV374906 PM3-HT130
	187	302.6	9.6	514	1	AA959087	AA959087 ua08f08.r
	188	302	9.6	388	6	CB779567	CB779567 AMGNNUC:N
	189	301	9.6	582	5	BP250593	BP250593 BP250593
	190	299.8	9.5	717	5	BM946956	BM946956 UI-M-EH0p
	191	298.6	9.5	583	5	BU694619	BU694619 LL2in1402
	192	298.4	9.5	437	2	BF605420	BF605420 271789 MA
	193	293.6	9.3	435	6	BY596404	BY596404 BY596404
	194	293.6	9.3	480	6	CB537061	CB537061 772134 MA
	195	293.6	9.3	512	1	AA510439	AA510439 vg32e04.r
c	196	293.2	9.3	303	7	T19440	T19440 f03002t Tes
	197	293	9.3	439	4	BM030747	BM030747 495245 MA
	198	289.6	9.2	689	1	AA274712	AA274712 vc15g11.r
	199	288.8	9.2	318	2	BE182018	BE182018 CM1-HT064
	200	288.2	9.2	368	2	AW632286	AW632286 92080 MAR
	201	287.6	9.2	655	2	BB621440	BB621440 BB621440
	202	287.2	9.1	475	4	BM286849	BM286849 527060 MA
	203	286.6	9.1	418	6	CB765926	CB765926 AMGNNUC:N
c	204	286.4	9.1	298	4	BM662404	BM662404 UI-E-CI1-
	205	285.8	9.1	481	7	W13797	W13797 ma94g12.r1
	206	285.8	9.1	514	9	CG646708	CG646708 OST393408
	207	285.6	9.1	354	2	BE155671	BE155671 PM2-HT035
	208	284.4	9.0	286	7	CN255816	CN255816 170005325
	209	283.6	9.0	398	2	BE014053	BE014053 125627 MA
	210	280.6	8.9	532	1	AA575453	AA575453 vl90b06.r
	211	279.4	8.9	285	7	CR736197	CR736197 CR736197
	212	279	8.9	512	2	BE012711	BE012711 122368 MA
c	213	273.6	8.7	343	7	R81500	R81500 yj05d01.s1
c	214	273.4	8.7	281	7	Z39973	Z39973 HSC10E102 n
	215	273	8.7	736	2	BE288736	BE288736 601093420
	216	271.4	8.6	327	7	Z43916	Z43916 HSC10E101 n
	217	269.4	8.6	636	6	BY745271	BY745271 BY745271
	218	261.6	8.3	385	6	CB702615	CB702615 AMGNNUC:S
	219	261.2	8.3	338	1	AA193482	AA193482 zr41d02.r
	220	257.4	8.2	507	2	BE668290	BE668290 156950 MA
	221	257.2	8.2	456	2	BB840212	BB840212 BB840212
	222	255	8.1	307	7	T34380	T34380 EST66751 Hu
	223	253	8.0	595	7	CN701121	CN701121 E0445B08-
	224	248.8	7.9	2480	9	AY407393	AY407393 Mus muscu
	225	248.6	7.9	343	2	AW446374	AW446374 85396 MAR
	226	247.8	7.9	407	5	BY201059	BY201059 BY201059
	227	247.4	7.9	339	7	CK942886	CK942886 4066584 B
	228	247.2	7.9	415	5	BY237094	BY237094 BY237094
	229	244	7.8	731	1	AI116589	AI116589 ue27f05.y
c	230	241.4	7.7	528	1	AI350408	AI350408 qt17b12.x
	231	241	7.7	330	2	AW483617	AW483617 55275 MAR
	232	240.6	7.7	3809	3	AK030331	AK030331 Mus muscu
	233	239	7.6	2777	3	AK028896	AK028896 Mus muscu
	234	234.8	7.5	548	5	BX515711	BX515711 BX515711
	235	233.6	7.4	517	2	BB867776	BB867776 BB867776
	236	233.2	7.4	359	5	BY344631	BY344631 BY344631

	237	233	7.4	529	1	AI119178	AI119178	ue23g10.y
c	238	232.2	7.4	259	1	AI698802	AI698802	wd31b11.x
	239	229.4	7.3	352	5	BY209243	BY209243	BY209243
	240	229.4	7.3	353	5	BY194675	BY194675	BY194675
	241	228.2	7.3	345	6	CB705908	CB705908	AMGNNUC:N
	242	227.6	7.2	2502	9	AY407391	AY407391	Homo sapi
	243	226.2	7.2	359	5	BY192032	BY192032	BY192032
	244	225.8	7.2	441	2	BB848500	BB848500	BB848500
	245	222.8	7.1	354	5	BY186467	BY186467	BY186467
c	246	222	7.1	226	1	AA971074	AA971074	op70g02.s
	247	220.6	7.0	399	5	BY258404	BY258404	BY258404
c	248	218.4	6.9	231	1	AA588098	AA588098	nm98h03.s
	249	218.4	6.9	356	5	BY203094	BY203094	BY203094
c	250	216.2	6.9	224	1	AA481169	AA481169	aa34h11.s
	251	216.2	6.9	555	7	CN699228	CN699228	E0418E11-
	252	216.2	6.9	925	5	BQ929233	BQ929233	AGENCOURT
	253	215.4	6.9	787	4	BI665818	BI665818	603289737
	254	213.4	6.8	978	5	BQ219389	BQ219389	AGENCOURT
	255	213.2	6.8	766	4	BI330594	BI330594	602981035
	256	212.8	6.8	344	5	BY182086	BY182086	BY182086
	257	212.4	6.8	342	5	BY190812	BY190812	BY190812
	258	212	6.7	554	1	AL780781	AL780781	AL780781
	259	211	6.7	3648	3	AK090073	AK090073	Mus muscu
	260	210.6	6.7	360	5	BY203098	BY203098	BY203098
	261	210	6.7	350	9	CG604636	CG604636	OST280536
	262	202.8	6.5	906	7	CF548431	CF548431	AGENCOURT
	263	201.6	6.4	361	6	BY780664	BY780664	BY780664
	264	199.4	6.3	340	5	BY180833	BY180833	BY180833
	265	198	6.3	904	2	BF134543	BF134543	601784950
	266	196.8	6.3	343	5	BY176481	BY176481	BY176481
	267	194.2	6.2	457	5	BY225325	BY225325	BY225325
	268	192	6.1	374	6	CB692309	CB692309	AMGNNUC:N
	269	191.8	6.1	398	5	BY284987	BY284987	BY284987
	270	191.6	6.1	691	7	CF767810	CF767810	CES006164
	271	190.6	6.1	298	2	BB586510	BB586510	BB586510
	272	190.4	6.1	380	5	BY265162	BY265162	BY265162
	273	189.8	6.0	424	5	BY188709	BY188709	BY188709
	274	189	6.0	386	5	BY231195	BY231195	BY231195
	275	186.6	5.9	267	4	BM485185	BM485185	539436 MA
	276	185.4	5.9	2502	9	AY407392	AY407392	Pan trogl
c	277	184.6	5.9	588	6	CB469303	CB469303	sn05_G02.
	278	181	5.8	504	2	BE481474	BE481474	166929 BA
	279	179.2	5.7	838	7	CF374334	CF374334	AGENCOURT
	280	176.4	5.6	416	5	BY183408	BY183408	BY183408
c	281	176	5.6	560	6	CB476226	CB476226	jns118_A0
	282	172.8	5.5	710	6	CB422627	CB422627	595748 MA
	283	170	5.4	312	5	BY170795	BY170795	BY170795
	284	169.2	5.4	782	5	BP684334	BP684334	BP684334
	285	166.8	5.3	297	5	BY000550	BY000550	BY000550
	286	165.8	5.3	356	5	BY233307	BY233307	BY233307
	287	163	5.2	411	6	BY547048	BY547048	BY547048
	288	163	5.2	437	7	CV312033	CV312033	CM0-PT004
	289	161.4	5.1	768	5	BM943605	BM943605	UI-M-EH0p
c	290	160.4	5.1	299	5	BQ356197	BQ356197	PM3-HT130
	291	158.2	5.0	724	4	BG716692	BG716692	602678071
	292	157	5.0	902	5	BQ933408	BQ933408	AGENCOURT
c	293	154.8	4.9	571	6	CB438091	CB438091	686532 MA

	294	154.6	4.9	473	4	BI775884	BI775884 468605 MA
	295	153.8	4.9	164	7	D45630	D45630 HUMGS02826
c	296	153.8	4.9	626	6	CB431656	CB431656 607652 MA
c	297	153.6	4.9	582	6	CB535123	CB535123 768510 MA
	298	153.2	4.9	863	1	AI323192	AI323192 mp55g10.y
	299	152	4.8	745	5	BM962964	BM962964 UI-M-EQ0-
c	300	151.6	4.8	172	2	AW467911	AW467911 he28c12.x
	301	150.2	4.8	780	7	CN255480	CN255480 170005312
	302	149.8	4.8	615	1	AL677440	AL677440 AL677440
	303	149	4.7	834	5	BQ216757	BQ216757 AGENCOURT
	304	146.4	4.7	977	5	BX370082	BX370082 BX370082
	305	146	4.6	211	4	BI345631	BI345631 374509 MA
	306	146	4.6	886	5	BQ943608	BQ943608 AGENCOURT
	307	145.8	4.6	448	2	BB847529	BB847529 BB847529
	308	145	4.6	416	2	AW430454	AW430454 70020 MAR
	309	143.8	4.6	615	6	CB437039	CB437039 684474 MA
	310	143.6	4.6	175	2	AW313646	AW313646 9051 MARC
	311	141.8	4.5	1068	4	BM811543	BM811543 AGENCOURT
	312	141.4	4.5	926	5	BU909663	BU909663 AGENCOURT
	313	141	4.5	706	7	CN255488	CN255488 170006001
	314	141	4.5	728	7	CN255483	CN255483 170005322
	315	141	4.5	864	4	BI518922	BI518922 603061844
	316	140	4.5	270	2	BB608272	BB608272 BB608272
	317	140	4.5	568	7	CN255489	CN255489 170005322
	318	136.8	4.4	443	5	BY167445	BY167445 BY167445
	319	136.4	4.3	580	2	BE752387	BE752387 204762 MA
	320	134	4.3	160	7	CO261051	CO261051 4133142 B
	321	134	4.3	948	5	BQ685036	BQ685036 AGENCOURT
	322	133	4.2	770	7	CO248318	CO248318 AGENCOURT
c	323	132.2	4.2	573	2	AW118237	AW118237 xe12b08.x
c	324	131.4	4.2	467	1	AV617760	AV617760 AV617760
	325	131.4	4.2	615	5	BM945001	BM945001 UI-M-EH0p
	326	130.4	4.1	563	6	CD216221	CD216221 pgp2n.pk0
	327	130.4	4.1	700	1	AA763586	AA763586 vp07g05.r
c	328	130	4.1	561	4	BM252112	BM252112 BOTL01000
	329	129.8	4.1	614	4	BG712158	BG712158 pg11n.pk0
	330	129.6	4.1	418	2	BE679181	BE679181 dc60b02.y
c	331	129.6	4.1	547	4	BM220500	BM220500 C0941F04-
c	332	129.6	4.1	598	2	BF714461	BF714461 mab01a06.
	333	129.6	4.1	700	6	BY763889	BY763889 BY763889
c	334	129.6	4.1	711	5	BP765487	BP765487 BP765487
c	335	129.6	4.1	773	1	AI132332	AI132332 ue23g10.x
c	336	129.6	4.1	780	7	CO040927	CO040927 UI-M-EV0-
	337	129.2	4.1	678	6	CA041134	CA041134 ssalshc50
	338	129.2	4.1	3763	3	AK088653	AK088653 Mus muscu
	339	128.8	4.1	708	7	CN789123	CN789123 4123542 B
	340	128.2	4.1	372	6	BY540732	BY540732 BY540732
	341	128	4.1	674	2	BB045065	BB045065 BB045065
	342	127.2	4.0	290	2	AW656129	AW656129 108203 MA
c	343	127	4.0	601	5	BP768508	BP768508 BP768508
	344	126.8	4.0	625	2	BE077531	BE077531 RC1-BT060
	345	126.6	4.0	342	1	AA611491	AA611491 vo89a05.r
	346	126.6	4.0	403	6	BY540418	BY540418 BY540418
	347	126.2	4.0	426	2	BB824296	BB824296 BB824296
	348	126.2	4.0	435	5	BY517409	BY517409 BY517409
	349	125.8	4.0	593	6	CD216085	CD216085 pgp2n.pk0
	350	125.6	4.0	387	5	BY504344	BY504344 BY504344

	351	125.6	4.0	410	5	BY510171	BY510171	BY510171
	352	125.6	4.0	422	5	BY494879	BY494879	BY494879
	353	125.4	4.0	455	7	CN223958	CN223958	WLA052D09
	354	125.2	4.0	306	2	AW436384	AW436384	76556 MAR
	355	125.2	4.0	344	1	AA611501	AA611501	vo89b04.r
	356	125.2	4.0	355	1	AA823216	AA823216	vw42b01.r
	357	125.2	4.0	366	2	BB792067	BB792067	BB792067
c	358	125.2	4.0	386	5	BX639014	BX639014	BX639014
c	359	125.2	4.0	396	2	BE851923	BE851923	uw18f07.x
	360	125.2	4.0	404	6	BY575062	BY575062	BY575062
	361	125.2	4.0	405	6	BY625364	BY625364	BY625364
	362	125.2	4.0	408	6	BY547045	BY547045	BY547045
	363	125.2	4.0	409	2	BB743231	BB743231	BB743231
	364	125.2	4.0	414	6	BY538798	BY538798	BY538798
	365	125.2	4.0	428	6	BY579800	BY579800	BY579800
	366	125.2	4.0	434	6	BY551281	BY551281	BY551281
	367	125.2	4.0	437	6	BY523338	BY523338	BY523338
c	368	125.2	4.0	441	2	AW061291	AW061291	UI-M-BH1-
	369	125.2	4.0	449	6	BY546162	BY546162	BY546162
	370	125.2	4.0	466	2	BB731279	BB731279	BB731279
	371	125.2	4.0	469	2	BB824926	BB824926	BB824926
	372	125.2	4.0	492	2	AW493316	AW493316	UI-M-BH3-
c	373	125.2	4.0	507	2	AW060306	AW060306	UI-M-BH1-
c	374	125.2	4.0	514	2	BF020082	BF020082	ux14b02.x
c	375	125.2	4.0	516	1	AI098213	AI098213	ue27f05.x
c	376	125.2	4.0	546	1	AI323581	AI323581	mp55g10.x
	377	125.2	4.0	910	5	BU552547	BU552547	AGENCOURT
	378	124.8	4.0	768	7	CN255481	CN255481	170005331
	379	124.4	4.0	372	5	BY236908	BY236908	BY236908
	380	124.2	4.0	387	5	BY511124	BY511124	BY511124
	381	124.2	4.0	685	6	CA371810	CA371810	652409 NC
	382	124	3.9	396	6	BY548006	BY548006	BY548006
c	383	124	3.9	446	1	AI606228	AI606228	vn98f09.x
	384	123.8	3.9	314	2	AW485003	AW485003	63380 MAR
	385	123.8	3.9	862	5	BQ224734	BQ224734	AGENCOURT
	386	123.6	3.9	399	6	BY541776	BY541776	BY541776
	387	123.6	3.9	410	5	BY513291	BY513291	BY513291
	388	123.6	3.9	433	5	BY498637	BY498637	BY498637
	389	123.6	3.9	660	2	BB126942	BB126942	BB126942
	390	123.6	3.9	853	7	CR574223	CR574223	CR574223
	391	123.4	3.9	319	2	BB317324	BB317324	BB317324
	392	123.2	3.9	406	5	BY516094	BY516094	BY516094
c	393	123.2	3.9	446	5	BP754487	BP754487	BP754487
	394	123.2	3.9	655	4	BJ618310	BJ618310	BJ618310
	395	123	3.9	330	2	BB164759	BB164759	BB164759
	396	123	3.9	446	2	BB820315	BB820315	BB820315
	397	122.8	3.9	236	2	BF776808	BF776808	288536 MA
	398	122.8	3.9	851	7	CF243117	CF243117	AGENCOURT
	399	122.8	3.9	880	5	BU541109	BU541109	AGENCOURT
	400	122.6	3.9	399	6	BY658194	BY658194	BY658194
	401	122.6	3.9	405	2	BB739127	BB739127	BB739127
	402	122.6	3.9	414	2	BE849780	BE849780	uw18f07.y
	403	122.6	3.9	417	5	BY516312	BY516312	BY516312
	404	122.6	3.9	432	6	BY525070	BY525070	BY525070
	405	122.6	3.9	445	2	BB779387	BB779387	BB779387
	406	122.4	3.9	399	5	BY183603	BY183603	BY183603
	407	122.4	3.9	401	5	BY507720	BY507720	BY507720

	408	122.2	3.9	343	2	BB222788	BB222788	BB222788
	409	122.2	3.9	415	6	BY646549	BY646549	BY646549
	410	122.2	3.9	420	6	BY524914	BY524914	BY524914
c	411	122.2	3.9	515	4	BM390926	BM390926	UI-R-CN1-
	412	122	3.9	347	2	BB113642	BB113642	BB113642
	413	122	3.9	402	5	BY507653	BY507653	BY507653
	414	121.8	3.9	314	1	AV235779	AV235779	AV235779
	415	121.8	3.9	548	2	BF039888	BF039888	BP250025A
	416	121.8	3.9	932	5	BX369159	BX369159	BX369159
	417	121.6	3.9	623	4	BJ095128	BJ095128	BJ095128
	418	121.6	3.9	881	4	BG824522	BG824522	602727494
c	419	121.4	3.9	651	4	BM385797	BM385797	UI-R-CN1-
	420	121.2	3.9	358	5	BY205630	BY205630	BY205630
	421	121.2	3.9	872	4	BG831590	BG831590	602765850
c	422	121	3.8	293	7	CO988317	CO988317	UMC-pd3en
c	423	121	3.8	387	2	BE690913	BE690913	uw60d09.x
	424	120.8	3.8	336	2	BB219364	BB219364	BB219364
	425	120.8	3.8	589	4	BI391274	BI391274	pgpln.pk0
	426	120.6	3.8	351	2	BE668250	BE668250	156853 MA
c	427	120.6	3.8	431	6	CA945768	CA945768	UI-R-FS1-
c	428	120.6	3.8	435	1	AI454122	AI454122	UI-R-BT0-
c	429	120.6	3.8	473	2	AW523699	AW523699	UI-R-BO0-
c	430	120.6	3.8	552	2	BE110750	BE110750	UI-R-BJ1-
c	431	120.6	3.8	555	5	BQ190381	BQ190381	UI-R-DN1-
c	432	120.6	3.8	649	6	CB322846	CB322846	UI-R-DY0-
	433	120.4	3.8	328	2	BB223967	BB223967	BB223967
	434	120.4	3.8	377	6	BY630131	BY630131	BY630131
	435	120.4	3.8	424	5	BY378169	BY378169	BY378169
c	436	120.4	3.8	528	5	BQ031863	BQ031863	UI-1-CF0-
c	437	120.2	3.8	381	7	CR468045	CR468045	CR468045
	438	120.2	3.8	446	1	AA254731	AA254731	mz80h03.r
	439	120.2	3.8	486	6	BY591764	BY591764	BY591764
c	440	120.2	3.8	656	4	BM251667	BM251667	BOTL01000
	441	120	3.8	324	2	BB503600	BB503600	BB503600
	442	120	3.8	904	5	BU543096	BU543096	AGENCOURT
	443	119.8	3.8	317	2	BB828413	BB828413	BB828413
	444	119.8	3.8	414	5	BY498892	BY498892	BY498892
	445	119.4	3.8	325	2	BB392255	BB392255	BB392255
	446	119.4	3.8	333	1	AA755192	AA755192	vq62b08.r
	447	119.4	3.8	447	6	BY539681	BY539681	BY539681
	448	119.2	3.8	329	2	BB321099	BB321099	BB321099
	449	119.2	3.8	961	5	BU542955	BU542955	AGENCOURT
	450	119	3.8	262	2	AW313948	AW313948	9649 MARC
	451	119	3.8	262	2	AW477528	AW477528	13351 MAR
	452	118.6	3.8	316	2	BB210291	BB210291	BB210291
	453	118.4	3.8	422	5	BY509778	BY509778	BY509778
	454	118.4	3.8	808	5	BU187281	BU187281	AGENCOURT
c	455	118.2	3.8	392	4	BI290997	BI290997	UI-R-DK0-
	456	118.2	3.8	670	7	CK834036	CK834036	4058164 B
	457	118.2	3.8	779	7	CF288502	CF288502	AGENCOURT
	458	118	3.8	373	5	BY017370	BY017370	BY017370
c	459	118	3.8	428	6	CB059945	CB059945	4010160 B
	460	118	3.8	763	5	BU612234	BU612234	UI-M-EW0-
	461	117.8	3.7	409	5	BY506868	BY506868	BY506868
	462	117.6	3.7	325	2	BB138812	BB138812	BB138812
	463	117.6	3.7	329	2	BB560121	BB560121	BB560121
	464	117.6	3.7	453	6	CB060019	CB060019	4010021 B

	465	117.6	3.7	654	5	BP754486	BP754486	BP754486
	466	117.4	3.7	504	1	AA110742	AA110742	mp55g10.r
	467	117.4	3.7	726	7	CK980025	CK980025	4111598 B
	468	117.2	3.7	336	2	BB165167	BB165167	BB165167
	469	117.2	3.7	407	5	BY516195	BY516195	BY516195
	470	117	3.7	149	6	CB062937	CB062937	4013191 B
	471	117	3.7	315	2	BB269712	BB269712	BB269712
	472	117	3.7	738	1	AL702888	AL702888	DKFZp686D
	473	117	3.7	917	5	BU916713	BU916713	AGENCOURT
	474	116.8	3.7	322	2	BB220489	BB220489	BB220489
	475	116.6	3.7	412	6	CB802007	CB802007	AMGNNUC:N
	476	116.6	3.7	426	2	AW767390	AW767390	da68e03.y
	477	116.6	3.7	711	7	CN401142	CN401142	170005328
	478	116.6	3.7	933	4	BG424061	BG424061	602448130
c	479	116.2	3.7	689	5	BX885697	BX885697	BX885697
	480	116	3.7	413	5	BY516984	BY516984	BY516984
	481	115.8	3.7	315	2	BB217943	BB217943	BB217943
	482	115.6	3.7	308	2	BB226784	BB226784	BB226784
	483	115.6	3.7	459	6	BY596859	BY596859	BY596859
	484	115.4	3.7	328	2	BB203677	BB203677	BB203677
	485	115	3.7	653	4	BG423200	BG423200	602450518
	486	115	3.7	1045	5	BX458922	BX458922	BX458922
	487	114.8	3.7	865	5	BQ962412	BQ962412	AGENCOURT
	488	114.6	3.6	413	6	BY577648	BY577648	BY577648
	489	114.4	3.6	318	2	BB221006	BB221006	BB221006
	490	114.4	3.6	3226	3	AK042751	AK042751	Mus muscu
	491	114.4	3.6	3329	3	AK082711	AK082711	Mus muscu
	492	114	3.6	268	2	BB594900	BB594900	BB594900
	493	113.8	3.6	552	7	CN664343	CN664343	A0811H09-
	494	113.4	3.6	408	5	BY159825	BY159825	BY159825
	495	113.4	3.6	1035	5	BQ944697	BQ944697	AGENCOURT
	496	113.2	3.6	262	2	BB733435	BB733435	BB733435
	497	113.2	3.6	297	2	BB082267	BB082267	BB082267
	498	113	3.6	294	2	BB369725	BB369725	BB369725
	499	113	3.6	311	2	BB319473	BB319473	BB319473
	500	113	3.6	647	4	BI159977	BI159977	602863854
	501	112.8	3.6	286	2	BB180038	BB180038	BB180038
	502	112.8	3.6	339	2	BB137126	BB137126	BB137126
	503	112.2	3.6	339	2	BB224502	BB224502	BB224502
	504	112.2	3.6	341	2	BB224286	BB224286	BB224286
	505	112.2	3.6	470	2	BB822561	BB822561	BB822561
	506	112	3.6	298	2	BB360425	BB360425	BB360425
	507	112	3.6	316	2	BB218778	BB218778	BB218778
	508	112	3.6	940	4	BG386070	BG386070	602455244
	509	111.8	3.6	287	2	BB179402	BB179402	BB179402
	510	111.8	3.6	395	5	BY019515	BY019515	BY019515
	511	111.8	3.6	691	4	BG422155	BG422155	602448882
	512	111.6	3.6	300	2	BB522135	BB522135	BB522135
	513	111.6	3.6	307	2	BB116702	BB116702	BB116702
	514	111.4	3.5	321	2	BB236584	BB236584	BB236584
	515	111.4	3.5	338	2	BB120467	BB120467	BB120467
	516	111.2	3.5	286	2	BB222636	BB222636	BB222636
	517	111.2	3.5	304	2	BB219012	BB219012	BB219012
	518	111.2	3.5	306	1	AV239830	AV239830	AV239830
	519	111.2	3.5	678	4	BM495316	BM495316	IpCGBr2_2
c	520	111.2	3.5	738	4	BM414643	BM414643	ECC00109
	521	111	3.5	277	2	BB324525	BB324525	BB324525

	522	110.8	3.5	295	2	BB511397	BB511397	BB511397
	523	110.6	3.5	1606	2	BF581604	BF581604	602099944
	524	110.4	3.5	788	4	BI161171	BI161171	602865624
	525	110.2	3.5	334	2	BB224542	BB224542	BB224542
	526	110	3.5	288	2	BB346214	BB346214	BB346214
	527	110	3.5	310	2	BB265127	BB265127	BB265127
c	528	110	3.5	344	1	AI070233	AI070233	UI-R-Y0-1
	529	109.8	3.5	306	2	BB530000	BB530000	BB530000
	530	109.8	3.5	487	7	CN367763	CN367763	170005322
	531	109.6	3.5	284	2	BB733429	BB733429	BB733429
	532	109.6	3.5	293	2	BB334189	BB334189	BB334189
	533	109.6	3.5	452	6	BY588670	BY588670	BY588670
	534	109.4	3.5	317	1	AV102365	AV102365	AV102365
	535	109.4	3.5	826	5	BU175920	BU175920	AGENCOURT
	536	109.4	3.5	1132	6	CD504092	CD504092	CDA66-A08
	537	109.2	3.5	357	5	BY193799	BY193799	BY193799
	538	109	3.5	110	6	CD631366	CD631366	56027747J
	539	109	3.5	292	2	BB440274	BB440274	BB440274
	540	109	3.5	295	2	BB179256	BB179256	BB179256
	541	109	3.5	298	2	BB257753	BB257753	BB257753
	542	108.8	3.5	309	2	BB124269	BB124269	BB124269
	543	108.8	3.5	310	2	BB335680	BB335680	BB335680
c	544	108.6	3.5	457	2	BE686664	BE686664	uw03e06.x
	545	108.4	3.4	292	2	BB173217	BB173217	BB173217
	546	108.4	3.4	299	2	BB276146	BB276146	BB276146
	547	108.2	3.4	168	2	AW345212	AW345212	25329 MAR
	548	108.2	3.4	311	2	BB143870	BB143870	BB143870
	549	108.2	3.4	910	4	BI161349	BI161349	602865754
	550	108	3.4	290	2	BB278479	BB278479	BB278479
	551	108	3.4	303	2	BB217218	BB217218	BB217218
	552	108	3.4	949	5	BU541977	BU541977	AGENCOURT
	553	108	3.4	3137	3	BC051979	BC051979	Mus muscu
	554	108	3.4	3907	3	AK031131	AK031131	Mus muscu
c	555	107.8	3.4	557	1	AU147993	AU147993	AU147993
	556	107.6	3.4	689	7	CO434547	CO434547	UI-M-HX0-
	557	107.6	3.4	1141	6	CA975355	CA975355	AGENCOURT
	558	107.4	3.4	289	2	BB007231	BB007231	BB007231
	559	107.4	3.4	305	2	BB500334	BB500334	BB500334
c	560	107.4	3.4	436	1	AA913136	AA913136	oi17h07.s
	561	107.4	3.4	569	7	CO258909	CO258909	4130136 B
c	562	107.4	3.4	734	5	BX674351	BX674351	BX674351
	563	107.2	3.4	312	2	BB445664	BB445664	BB445664
	564	107	3.4	284	2	BB507939	BB507939	BB507939
	565	106.8	3.4	289	2	BB496529	BB496529	BB496529
	566	106.8	3.4	290	2	BB368263	BB368263	BB368263
	567	106.8	3.4	292	2	BB354765	BB354765	BB354765
	568	106.8	3.4	304	2	BB336700	BB336700	BB336700
	569	106.8	3.4	328	2	BB220954	BB220954	BB220954
	570	106.6	3.4	686	4	BG469296	BG469296	602533135
	571	106.4	3.4	279	2	BB371226	BB371226	BB371226
	572	106.4	3.4	286	2	BB555504	BB555504	BB555504
	573	106.4	3.4	294	1	AV051876	AV051876	AV051876
	574	106.4	3.4	336	2	AW226731	AW226731	um60b09.y
c	575	106.4	3.4	488	4	BM151697	BM151697	TCBAP1E10
	576	106.2	3.4	281	2	BB346087	BB346087	BB346087
	577	106.2	3.4	725	7	CN429157	CN429157	170004252
	578	106	3.4	306	2	BB262651	BB262651	BB262651

579	106	3.4	318	2	BB243620	BB243620	BB243620
580	105.8	3.4	272	2	BB552255	BB552255	BB552255
581	105.8	3.4	283	2	BB128450	BB128450	BB128450
582	105.8	3.4	292	2	BB500569	BB500569	BB500569
583	105.8	3.4	976	5	BQ944147	BQ944147	AGENCOURT
584	105.6	3.4	281	2	BB348185	BB348185	BB348185
585	105.6	3.4	811	6	CD653578	CD653578	AGENCOURT
586	105.6	3.4	824	4	BM047429	BM047429	603628715
587	105.6	3.4	900	4	BG326356	BG326356	602425281
588	105.4	3.4	363	6	CD631362	CD631362	56027755J
c 589	105.4	3.4	603	7	CK849657	CK849657	972704 BA
c 590	105.4	3.4	742	5	BX910552	BX910552	BX910552
591	105.2	3.3	287	2	BB325091	BB325091	BB325091
592	105	3.3	394	6	CB776364	CB776364	AMGNNUC:N
593	105	3.3	860	5	BQ230111	BQ230111	AGENCOURT
594	105	3.3	924	4	BG326746	BG326746	602425623
595	105	3.3	963	5	BU552403	BU552403	AGENCOURT
596	105	3.3	1024	2	BE910319	BE910319	601503675
597	104.8	3.3	262	1	AV241169	AV241169	AV241169
598	104.8	3.3	306	2	BB500200	BB500200	BB500200
599	104.8	3.3	414	2	BB826095	BB826095	BB826095
600	104.8	3.3	795	6	CB245479	CB245479	UI-M-FY0-
601	104.8	3.3	911	5	BU501900	BU501900	AGENCOURT
602	104.8	3.3	919	5	BU173969	BU173969	AGENCOURT
603	104.6	3.3	282	2	BB532703	BB532703	BB532703
604	104.6	3.3	309	2	BB499049	BB499049	BB499049
605	104.2	3.3	310	2	BB236046	BB236046	BB236046
606	104.2	3.3	328	2	BB114323	BB114323	BB114323
607	104.2	3.3	414	6	BY578439	BY578439	BY578439
608	104.2	3.3	897	5	BQ219988	BQ219988	AGENCOURT
609	104.2	3.3	927	4	BG831583	BG831583	602765840
610	104	3.3	266	2	BB716868	BB716868	BB716868
611	104	3.3	283	2	BB528644	BB528644	BB528644
612	104	3.3	288	2	BB342818	BB342818	BB342818
613	104	3.3	2855	3	AK047067	AK047067	Mus muscu
614	103.8	3.3	298	2	BB283107	BB283107	BB283107
615	103.8	3.3	879	4	BG831929	BG831929	602765589
616	103.6	3.3	297	2	BB217129	BB217129	BB217129
617	103.6	3.3	307	2	BB500311	BB500311	BB500311
618	103.6	3.3	311	2	BB533042	BB533042	BB533042
619	103.6	3.3	315	2	BB122455	BB122455	BB122455
620	103.6	3.3	464	2	BB796655	BB796655	BB796655
621	103.4	3.3	314	2	BB239048	BB239048	BB239048
622	103.2	3.3	233	2	BB510804	BB510804	BB510804
623	103.2	3.3	286	2	BB178968	BB178968	BB178968
624	103.2	3.3	467	6	BY556536	BY556536	BY556536
625	103.2	3.3	583	4	BM488072	BM488072	pgm2n.pk0
626	103.2	3.3	868	1	AU140366	AU140366	AU140366
627	103	3.3	282	2	BB310767	BB310767	BB310767
628	103	3.3	619	1	AL118624	AL118624	DKFZp761F
629	102.8	3.3	269	2	BB313946	BB313946	BB313946
630	102.6	3.3	271	2	BB216188	BB216188	BB216188
631	102.6	3.3	579	5	BP375801	BP375801	BP375801
632	102.6	3.3	869	5	BM947242	BM947242	UI-M-EH0p
633	102.6	3.3	977	5	BU520216	BU520216	AGENCOURT
634	102.4	3.3	281	2	BB129002	BB129002	BB129002
635	102.2	3.3	268	2	BB216101	BB216101	BB216101

	636	102.2	3.3	271	2	BB555572	BB555572	BB555572
	637	102.2	3.3	285	2	BB324617	BB324617	BB324617
	638	102.2	3.3	342	2	BB223376	BB223376	BB223376
	639	102.2	3.3	644	1	AL803713	AL803713	AL803713
	640	102.2	3.3	659	7	CN695559	CN695559	E0366G09-
c	641	102	3.2	331	1	AI228417	AI228417	EST225112
	642	102	3.2	426	5	BY376368	BY376368	BY376368
c	643	102	3.2	654	6	CB420254	CB420254	593189 MA
	644	102	3.2	6875	3	BC032619	BC032619	Homo sapi
	645	101.8	3.2	222	2	BB150791	BB150791	BB150791
c	646	101.8	3.2	353	8	BZ845553	BZ845553	CH240_213
c	647	101.8	3.2	538	8	AQ434948	AQ434948	HS_5126_B
	648	101.8	3.2	779	5	BX396978	BX396978	BX396978
	649	101.8	3.2	1002	5	BQ068313	BQ068313	AGENCOURT
	650	101.6	3.2	315	2	BB116770	BB116770	BB116770
c	651	101.6	3.2	537	2	BE349814	BE349814	hq43e01.x
	652	101.2	3.2	317	2	BB213717	BB213717	BB213717
	653	101	3.2	254	2	BB172165	BB172165	BB172165
	654	101	3.2	2719	3	AK035993	AK035993	Mus muscu
	655	100.8	3.2	400	6	BY555199	BY555199	BY555199
c	656	100.8	3.2	492	1	AA023538	AA023538	mh75d07.r
	657	100.8	3.2	622	6	CD349441	CD349441	UI-M-FY0-
	658	100.6	3.2	505	4	BI898654	BI898654	479668 MA
	659	100.6	3.2	651	4	BM491746	BM491746	pgp2n.pk0
	660	100.4	3.2	285	2	BB177820	BB177820	BB177820
	661	100.2	3.2	699	4	BG830948	BG830948	602766844
	662	100.2	3.2	861	7	CO735048	CO735048	SlLE04c10
	663	100	3.2	224	2	BB499666	BB499666	BB499666
	664	100	3.2	286	2	BB110106	BB110106	BB110106
	665	100	3.2	316	2	BB145363	BB145363	BB145363
c	666	100	3.2	582	2	BF400607	BF400607	UI-R-CA0-
	667	100	3.2	786	7	CK365293	CK365293	AGENCOURT
	668	99.8	3.2	313	2	BB218103	BB218103	BB218103
	669	99.8	3.2	594	7	CN528682	CN528682	UI-M-HQ0-
	670	99.8	3.2	910	4	BG470201	BG470201	602533710
	671	99.8	3.2	3921	3	AK084922	AK084922	Mus muscu
	672	99.8	3.2	4374	3	AK031307	AK031307	Mus muscu
c	673	99.6	3.2	278	6	CD631370	CD631370	56027863J
c	674	99.6	3.2	703	1	AU170734	AU170734	AU170734
	675	99.6	3.2	844	7	CO735027	CO735027	SlLE04c10
	676	99.6	3.2	880	5	BU186709	BU186709	AGENCOURT
	677	99.4	3.2	286	2	BB333313	BB333313	BB333313
	678	99.4	3.2	772	4	BG829652	BG829652	602764012
	679	99.2	3.2	275	2	BB227524	BB227524	BB227524
	680	99.2	3.2	326	2	BB559836	BB559836	BB559836
	681	99	3.1	239	1	AV229642	AV229642	AV229642
	682	99	3.1	264	1	AV238667	AV238667	AV238667
	683	99	3.1	316	2	BB532106	BB532106	BB532106
c	684	99	3.1	319	4	BG377549	BG377549	UI-R-CU0-
	685	98.6	3.1	121	1	AI264258	AI264258	qk20b04.x
	686	98.6	3.1	278	2	BB176510	BB176510	BB176510
	687	98.6	3.1	317	1	AL655823	AL655823	AL655823
	688	98.4	3.1	100	4	BI002468	BI002468	MR3-HN015
	689	98.4	3.1	228	2	BB150964	BB150964	BB150964
	690	98.4	3.1	288	2	BB455324	BB455324	BB455324
	691	98.4	3.1	320	2	BB242404	BB242404	BB242404
	692	98.2	3.1	278	1	AV313234	AV313234	AV313234

693	98.2	3.1	308	2	BB263999	BB263999	BB263999
694	98.2	3.1	668	6	BY746861	BY746861	BY746861
695	98.2	3.1	4476	3	AK052232	AK052232	Mus muscu
696	98	3.1	235	2	BB716819	BB716819	BB716819
697	98	3.1	280	2	BB535881	BB535881	BB535881
698	97.6	3.1	203	4	BM105287	BM105287	508710 MA
699	97.6	3.1	369	5	BY020398	BY020398	BY020398
700	97.4	3.1	705	2	BE294211	BE294211	601172744
701	97.2	3.1	256	2	BB425457	BB425457	BB425457
702	97.2	3.1	281	1	AV235738	AV235738	AV235738
703	97.2	3.1	640	7	CN460578	CN460578	UI-M-HB0-
704	97.2	3.1	704	6	BY741417	BY741417	BY741417
705	96.8	3.1	223	1	AV229388	AV229388	AV229388
706	96.8	3.1	225	2	BB323996	BB323996	BB323996
707	96.8	3.1	236	2	BB019685	BB019685	BB019685
708	96.8	3.1	242	2	BB554948	BB554948	BB554948
709	96.8	3.1	273	2	BB010623	BB010623	BB010623
710	96.8	3.1	286	2	BB309932	BB309932	BB309932
711	96.8	3.1	496	7	CK390327	CK390327	K0817F12-
712	96.8	3.1	815	4	BG386811	BG386811	602455071
713	96.8	3.1	986	4	BG746534	BG746534	602703833
714	96.8	3.1	1394	5	BM926974	BM926974	AGENCOURT
715	96.6	3.1	234	2	BB357534	BB357534	BB357534
716	96.6	3.1	340	5	BY353322	BY353322	BY353322
717	96.6	3.1	342	2	BB241607	BB241607	BB241607
718	96.6	3.1	352	5	BY177856	BY177856	BY177856
719	96.6	3.1	396	5	BY201883	BY201883	BY201883
720	96.6	3.1	795	7	CO571948	CO571948	AGENCOURT
721	96.4	3.1	721	6	CA324424	CA324424	UI-M-FY0-
722	96.4	3.1	779	6	CA316005	CA316005	UI-M-FW0-
c 723	96.2	3.1	297	1	AI112352	AI112352	UI-R-Y0-m
c 724	96.2	3.1	297	1	AI576402	AI576402	UI-R-Y0-v
725	96.2	3.1	333	1	AV006222	AV006222	AV006222
726	96	3.1	400	5	BY158515	BY158515	BY158515
727	96	3.1	917	4	BG324311	BG324311	602423309
728	95.8	3.0	586	2	BF041445	BF041445	BP250015B
729	95.8	3.0	673	5	BM951984	BM951984	UI-M-EH0-
c 730	95.8	3.0	710	7	CK979615	CK979615	4111214 B
731	95.4	3.0	178	2	BF774071	BF774071	283623 MA
732	95.4	3.0	178	2	BF774072	BF774072	283624 MA
733	95.4	3.0	222	2	BB052672	BB052672	BB052672
734	95.4	3.0	238	2	BB034746	BB034746	BB034746
735	95.4	3.0	261	2	BB594935	BB594935	BB594935
736	95.4	3.0	278	2	BB173822	BB173822	BB173822
737	95.4	3.0	281	2	BB108075	BB108075	BB108075
738	95.4	3.0	436	5	BY487960	BY487960	BY487960
739	95.2	3.0	227	2	BB501238	BB501238	BB501238
740	95.2	3.0	243	1	AV232151	AV232151	AV232151
741	95.2	3.0	246	2	BB301620	BB301620	BB301620
742	95.2	3.0	297	2	BB135944	BB135944	BB135944
743	95.2	3.0	325	2	BB218380	BB218380	BB218380
c 744	95.2	3.0	434	4	BM193462	BM193462	TCBAP1Q13
745	95.2	3.0	490	1	AI365650	AI365650	ap20h08.x
746	95	3.0	380	5	BY165728	BY165728	BY165728
747	95	3.0	459	2	BB633829	BB633829	BB633829
748	95	3.0	519	2	BF046214	BF046214	BP250021A
749	95	3.0	541	2	BF045972	BF045972	BP250003B

	750	95	3.0	542	2	BF039059	BF039059	BP250018B
	751	95	3.0	648	6	CB419189	CB419189	592037 MA
	752	94.8	3.0	336	2	BB241589	BB241589	BB241589
	753	94.8	3.0	710	6	CA379066	CA379066	658061 NC
	754	94.8	3.0	4045	3	BC059007	BC059007	Mus muscu
	755	94.6	3.0	248	1	AV326941	AV326941	AV326941
	756	94.6	3.0	267	2	BB108706	BB108706	BB108706
	757	94.6	3.0	278	2	BB479760	BB479760	BB479760
	758	94.6	3.0	281	2	BB221528	BB221528	BB221528
	759	94.6	3.0	531	2	BE235013	BE235013	142239 MA
	760	94.6	3.0	703	5	BM951868	BM951868	UI-M-EH0-
	761	94.4	3.0	275	2	BB336194	BB336194	BB336194
	762	94.4	3.0	291	1	AV339535	AV339535	AV339535
	763	94.4	3.0	336	2	BB497526	BB497526	BB497526
	764	94.4	3.0	520	7	CN255484	CN255484	170005313
	765	94.4	3.0	954	4	BG829919	BG829919	602764325
	766	94.2	3.0	211	2	BB591302	BB591302	BB591302
	767	94.2	3.0	481	7	CK392759	CK392759	K0849F03-
	768	94.2	3.0	690	6	BY734086	BY734086	BY734086
	769	94.2	3.0	819	6	CD628635	CD628635	56097918H
c	770	94.2	3.0	828	5	BX665346	BX665346	BX665346
	771	94	3.0	230	2	BB254403	BB254403	BB254403
	772	94	3.0	301	2	BB335163	BB335163	BB335163
	773	94	3.0	589	4	BM150494	BM150494	TCBAP1D10
	774	93.8	3.0	227	2	BB213341	BB213341	BB213341
	775	93.8	3.0	249	2	BB324195	BB324195	BB324195
	776	93.8	3.0	575	2	BE245715	BE245715	TCBAP1D19
	777	93.6	3.0	225	2	BB270419	BB270419	BB270419
	778	93.6	3.0	229	2	BB217995	BB217995	BB217995
	779	93.6	3.0	237	2	BB431741	BB431741	BB431741
	780	93.6	3.0	238	2	BB356581	BB356581	BB356581
	781	93.6	3.0	239	1	AV238091	AV238091	AV238091
	782	93.6	3.0	241	1	AV341229	AV341229	AV341229
	783	93.6	3.0	241	2	BB073528	BB073528	BB073528
	784	93.6	3.0	254	2	BB258946	BB258946	BB258946
	785	93.6	3.0	259	2	BB215951	BB215951	BB215951
	786	93.6	3.0	478	2	BF654570	BF654570	278796 MA
	787	93.4	3.0	244	2	BB519336	BB519336	BB519336
	788	93.2	3.0	146	4	BI847990	BI847990	470271 MA
	789	93.2	3.0	244	2	BB242763	BB242763	BB242763
	790	93.2	3.0	265	1	AV286945	AV286945	AV286945
c	791	93.2	3.0	515	1	AL928354	AL928354	AL928354
	792	93.2	3.0	2340	9	AY421319	AY421319	Mus muscu
	793	93.2	3.0	3159	3	AK046502	AK046502	Mus muscu
	794	93.2	3.0	3225	9	AY400493	AY400493	Mus muscu
	795	93.2	3.0	3726	3	AK043386	AK043386	Mus muscu
	796	93	3.0	231	2	BB151727	BB151727	BB151727
	797	93	3.0	527	2	BF462568	BF462568	UI-M-CG0p
	798	93	3.0	725	6	CB520645	CB520645	UI-M-GI0-
	799	92.6	2.9	198	4	BI021066	BI021066	PM3-MT020
	800	92.6	2.9	228	2	BB073945	BB073945	BB073945
	801	92.6	2.9	289	2	BB720615	BB720615	BB720615
	802	92.6	2.9	377	5	BY165251	BY165251	BY165251
	803	92.6	2.9	546	6	CA406911	CA406911	1003060 H
	804	92.6	2.9	2575	3	AK031231	AK031231	Mus muscu
	805	92.4	2.9	274	2	BB177348	BB177348	BB177348
c	806	92.4	2.9	404	4	BM174889	BM174889	hippo_08_

807	92.2	2.9	587	5	BP214222	BP214222	BP214222
808	92.2	2.9	691	5	BM944530	BM944530	UI-M-EH0p
809	92	2.9	239	2	BB356352	BB356352	BB356352
810	92	2.9	274	2	BB551851	BB551851	BB551851
811	92	2.9	343	2	BB224139	BB224139	BB224139
812	92	2.9	492	7	CN333872	CN333872	170005325
813	92	2.9	518	2	BF714462	BF714462	mab01a06.
814	92	2.9	748	7	CN333873	CN333873	170006000
815	91.8	2.9	593	7	CN255490	CN255490	170006000
816	91.8	2.9	734	7	CO395136	CO395136	AGENCOURT
817	91.8	2.9	918	7	CF780707	CF780707	AGENCOURT
818	91.6	2.9	247	2	BB170802	BB170802	BB170802
c 819	91.6	2.9	434	1	AV608925	AV608925	AV608925
820	91.6	2.9	704	6	CB527136	CB527136	UI-M-FY0-
821	91.6	2.9	937	5	BU518484	BU518484	AGENCOURT
822	91.4	2.9	433	6	BY580507	BY580507	BY580507
823	91.4	2.9	600	5	BU925145	BU925145	7112-63 M
824	91.2	2.9	281	6	CD631369	CD631369	56027863H
825	91.2	2.9	543	6	CD216128	CD216128	pgp2n.pk0
826	91.2	2.9	756	4	BI645497	BI645497	603275463
827	91	2.9	229	1	AV232333	AV232333	AV232333
828	91	2.9	625	6	CB247662	CB247662	UI-M-FI0-
829	91	2.9	740	7	CF532104	CF532104	UI-M-FY0-
c 830	90.8	2.9	228	6	CB168395	CB168395	HSF603268
831	90.8	2.9	657	7	CN788571	CN788571	4122921 B
832	90.6	2.9	283	1	AV224722	AV224722	AV224722
833	90.6	2.9	827	4	BF981141	BF981141	602310407
834	90.4	2.9	230	2	BB270171	BB270171	BB270171
835	90.4	2.9	239	2	BB267673	BB267673	BB267673
836	90.4	2.9	369	5	BY170960	BY170960	BY170960
837	90.2	2.9	238	2	BB356191	BB356191	BB356191
838	89.8	2.9	235	2	BB170781	BB170781	BB170781
839	89.8	2.9	245	2	BB149370	BB149370	BB149370
840	89.8	2.9	896	4	BI457032	BI457032	603185949
841	89.6	2.9	279	2	BB177200	BB177200	BB177200
842	89.4	2.8	256	7	CN223998	CN223998	WLA052F08
843	89.4	2.8	574	5	BM946983	BM946983	UI-M-EH0p
844	89.2	2.8	329	2	BB499916	BB499916	BB499916
845	89	2.8	231	2	BB148551	BB148551	BB148551
846	89	2.8	255	2	BB001987	BB001987	BB001987
847	89	2.8	456	5	BY491040	BY491040	BY491040
848	89	2.8	509	2	AW964929	AW964929	EST376897
849	88.8	2.8	228	2	BB341090	BB341090	BB341090
850	88.8	2.8	232	2	BB009287	BB009287	BB009287
851	88.6	2.8	593	5	BP249762	BP249762	BP249762
c 852	88.6	2.8	873	5	BX770216	BX770216	BX770216
853	88.2	2.8	567	4	BG710581	BG710581	pglln.pk0
854	88	2.8	282	2	BB531669	BB531669	BB531669
855	88	2.8	745	6	CA388534	CA388534	670926 NC
856	87.8	2.8	256	5	BM948107	BM948107	UI-M-EG0p
857	87.8	2.8	824	4	BI161136	BI161136	602865179
858	87.4	2.8	229	2	BB173708	BB173708	BB173708
859	87.4	2.8	234	2	BB717863	BB717863	BB717863
860	87.4	2.8	340	5	BY207534	BY207534	BY207534
861	87.4	2.8	745	5	BU055918	BU055918	UI-M-FO0-
862	87.2	2.8	229	2	BB239543	BB239543	BB239543
863	87.2	2.8	240	2	BB326658	BB326658	BB326658

864	87	2.8	697	2	AW134401	AW134401	fi18h09.y
865	87	2.8	770	6	CD628629	CD628629	56097478H
866	86.8	2.8	242	2	BB359459	BB359459	BB359459
867	86.8	2.8	258	1	AV375018	AV375018	AV375018
868	86.6	2.8	433	5	BY376940	BY376940	BY376940
869	86.6	2.8	917	2	BE908445	BE908445	601503077
870	86.6	2.8	923	4	BI665624	BI665624	603289613
871	86.6	2.8	2376	3	AK045236	AK045236	Mus muscu
872	86.4	2.7	216	2	BB323957	BB323957	BB323957
873	86.4	2.7	462	6	CD553207	CD553207	B0356E10-
874	86.4	2.7	621	4	BM738310	BM738310	K-EST0003
875	86.4	2.7	631	6	BY724321	BY724321	BY724321
876	86.4	2.7	632	2	BE270240	BE270240	601186027
c 877	86.4	2.7	646	2	BF322402	BF322402	maa24f04.
878	86.4	2.7	966	5	BQ715428	BQ715428	AGENCOURT
879	86.2	2.7	208	2	BB079119	BB079119	BB079119
880	86.2	2.7	242	1	AV381879	AV381879	AV381879
881	86.2	2.7	249	2	BB215799	BB215799	BB215799
882	86.2	2.7	929	5	BQ917819	BQ917819	AGENCOURT
883	86	2.7	211	2	BB184958	BB184958	BB184958
884	86	2.7	280	2	BB142942	BB142942	BB142942
885	86	2.7	570	2	BE407695	BE407695	601299714
886	85.8	2.7	543	2	AW966670	AW966670	EST378744
887	85.8	2.7	757	4	BI735927	BI735927	603360340
888	85.6	2.7	224	2	BB171694	BB171694	BB171694
889	85.6	2.7	245	1	AV232593	AV232593	AV232593
890	85.6	2.7	673	7	CN401143	CN401143	170005322
891	85.6	2.7	900	6	CA321459	CA321459	UI-M-FW0-
892	85.6	2.7	965	5	BU845252	BU845252	AGENCOURT
893	85.6	2.7	977	5	BU855862	BU855862	AGENCOURT
894	85.4	2.7	284	2	BB181557	BB181557	BB181557
895	85.4	2.7	356	5	BY204763	BY204763	BY204763
896	85.4	2.7	515	2	BB633428	BB633428	BB633428
897	85.2	2.7	207	2	BB214019	BB214019	BB214019
898	85.2	2.7	620	5	BM943707	BM943707	UI-M-EH0p
899	85	2.7	306	2	BB030476	BB030476	BB030476
900	84.6	2.7	232	2	BB262137	BB262137	BB262137
901	84.6	2.7	264	2	BB534094	BB534094	BB534094
902	84.6	2.7	266	2	BB196113	BB196113	BB196113
903	84.6	2.7	698	5	BU227771	BU227771	603800481
904	84.4	2.7	628	6	CA318117	CA318117	UI-M-FW0-
905	84.4	2.7	1010	5	BX360753	BX360753	BX360753
906	84.4	2.7	1246	2	BF166143	BF166143	601776590
907	84.2	2.7	218	2	BB213301	BB213301	BB213301
908	84	2.7	456	5	BY155480	BY155480	BY155480
909	84	2.7	790	6	CB248961	CB248961	UI-M-EX0-
910	84	2.7	864	5	BU156223	BU156223	AGENCOURT
911	83.8	2.7	214	2	BB588963	BB588963	BB588963
912	83.6	2.7	249	1	AV381817	AV381817	AV381817
913	83.4	2.7	270	2	BB177951	BB177951	BB177951
914	83.4	2.7	720	6	CD628637	CD628637	56098002H
915	83.4	2.7	777	6	CB248692	CB248692	UI-M-EX0-
916	83	2.6	227	2	BB216867	BB216867	BB216867
c 917	83	2.6	338	6	CB060198	CB060198	4010590 B
918	83	2.6	691	5	BQ180084	BQ180084	UI-M-EW0-
919	82.8	2.6	334	5	BY023564	BY023564	BY023564
920	82.8	2.6	425	1	AV665430	AV665430	AV665430

	921	82.8	2.6	511	6	CA383610	CA383610	663812	NC
	922	82.8	2.6	647	5	BM950623	BM950623	UI-M-EH0p	
	923	82.6	2.6	410	5	BU428839	BU428839	UI-HF-BN0	
	924	82.6	2.6	445	2	BE244550	BE244550	TCBAP1D11	
	925	82.6	2.6	492	2	BE018639	BE018639	bb83a12.y	
	926	82.6	2.6	549	2	AW655369	AW655369	106098	MA
	927	82.6	2.6	638	2	AW245910	AW245910	2822888.5	
c	928	82.4	2.6	139	7	CK942460	CK942460	4066200	B
	929	82.4	2.6	227	2	BB221591	BB221591	BB221591	
	930	82.4	2.6	569	2	AW499893	AW499893	UI-HF-BN0	
	931	82.4	2.6	582	5	BP348794	BP348794	BP348794	
	932	82	2.6	200	6	BY589580	BY589580	BY589580	
	933	82	2.6	224	2	BB170950	BB170950	BB170950	
	934	82	2.6	314	5	BY347200	BY347200	BY347200	
	935	82	2.6	855	5	BQ770087	BQ770087	UI-M-FI0-	
	936	81.8	2.6	228	1	AV231620	AV231620	AV231620	
c	937	81.6	2.6	377	2	BE246473	BE246473	TCBAP1E47	
	938	81.4	2.6	2292	9	AY402638	AY402638	Mus muscu	
	939	81.2	2.6	707	6	BY733150	BY733150	BY733150	
	940	81.2	2.6	821	7	CK846765	CK846765	969310	MA
	941	81	2.6	553	7	CN684594	CN684594	E0195H06-	
	942	80.8	2.6	378	2	BB745658	BB745658	BB745658	
	943	80.8	2.6	459	4	BJ043336	BJ043336	BJ043336	
	944	80.8	2.6	479	2	BF731124	BF731124	mab81e06.	
	945	80.4	2.6	240	2	BB301102	BB301102	BB301102	
	946	80.4	2.6	405	6	CB808856	CB808856	AMGNNUC:S	
	947	80.4	2.6	625	6	CD348364	CD348364	UI-M-FY0-	
c	948	80.4	2.6	763	6	CD619057	CD619057	56030577H	
	949	80.4	2.6	785	4	BI194687	BI194687	602946246	
	950	80.4	2.6	797	7	CO404183	CO404183	AGENCOURT	
	951	80.4	2.6	890	5	BU856543	BU856543	AGENCOURT	
	952	80.2	2.6	363	5	BY344602	BY344602	BY344602	
	953	80.2	2.6	850	5	BM944264	BM944264	UI-M-EH0p	
	954	80.2	2.6	900	7	CK799299	CK799299	AGENCOURT	
c	955	79.8	2.5	307	4	BF961259	BF961259	PM1-NN120	
	956	79.8	2.5	700	6	CD628633	CD628633	56097902H	
	957	79.6	2.5	233	2	BB134411	BB134411	BB134411	
	958	79.6	2.5	237	2	BB593564	BB593564	BB593564	
	959	79.6	2.5	268	2	BB383954	BB383954	BB383954	
c	960	79.6	2.5	426	4	BF954455	BF954455	MR4-NN020	
	961	79.6	2.5	718	4	BG475468	BG475468	602491461	
	962	79.6	2.5	801	5	BX313585	BX313585	BX313585	
	963	79.6	2.5	922	5	BQ943695	BQ943695	AGENCOURT	
	964	79.6	2.5	2349	9	AY421317	AY421317	Homo sapi	
	965	79.4	2.5	581	5	BX310430	BX310430	BX310430	
	966	79.4	2.5	643	5	BX087763	BX087763	BX087763	
	967	79.2	2.5	362	5	BY344235	BY344235	BY344235	
c	968	79.2	2.5	457	2	AW462107	AW462107	BP230008A	
	969	79.2	2.5	647	2	BE907509	BE907509	601497468	
	970	79	2.5	295	2	BB354856	BB354856	BB354856	
	971	79	2.5	453	2	AW500044	AW500044	UI-HF-BN0	
	972	79	2.5	593	5	BQ266902	BQ266902	NISC_ff15	
	973	79	2.5	978	5	BQ963608	BQ963608	AGENCOURT	
	974	78.8	2.5	696	7	CK974651	CK974651	4105581	B
	975	78.8	2.5	826	6	CD628641	CD628641	56097486H	
	976	78.6	2.5	474	2	AW659439	AW659439	96609	MAR
c	977	78.6	2.5	599	2	BF357811	BF357811	RC2-LT000	

978	78.4	2.5	450	2	BE653346	BE653346	UI-M-AL1-
979	78.4	2.5	490	6	CA531840	CA531840	C0325D06-
980	78.4	2.5	645	7	CF170234	CF170234	B0824E08-
981	78.4	2.5	696	7	CF168782	CF168782	B0804F02-
982	78.4	2.5	719	7	CK636248	CK636248	UI-M-HN0-
983	78.2	2.5	225	2	BB443283	BB443283	BB443283
984	78.2	2.5	231	2	BB148230	BB148230	BB148230
c 985	78.2	2.5	254	6	CB469624	CB469624	sn09_H09.
986	78	2.5	239	2	BB109818	BB109818	BB109818
987	77.8	2.5	219	1	AV369146	AV369146	AV369146
c 988	77.8	2.5	551	2	BF516420	BF516420	UI-H-BW1-
989	77.6	2.5	175	1	AV375624	AV375624	AV375624
990	77.2	2.5	887	5	BU906435	BU906435	AGENCOURT
c 991	77	2.4	703	5	BM936326	BM936326	UI-M-CG0p
992	76.8	2.4	438	7	CF535009	CF535009	UI-M-GH0-
993	76.8	2.4	687	4	BG327618	BG327618	602426612
994	76.6	2.4	357	1	AI877089	AI877089	vz73g04.r
995	76.6	2.4	443	4	BM484413	BM484413	538266 MA
996	76.6	2.4	469	7	CN429211	CN429211	170005327
997	76.6	2.4	862	1	AU118557	AU118557	AU118557
c 998	76.4	2.4	106	6	CD631365	CD631365	56027747H
999	76.2	2.4	234	1	AV250428	AV250428	AV250428
1000	76.2	2.4	904	5	BU145486	BU145486	AGENCOURT
1001	76.2	2.4	2224	9	AY421318	AY421318	Pan trogl
1002	76	2.4	77	6	CD631368	CD631368	56027839J
1003	76	2.4	223	2	BB330942	BB330942	BB330942
1004	76	2.4	283	6	CD631364	CD631364	56027739J
1005	76	2.4	600	4	BI986000	BI986000	3154-38 M
1006	75.8	2.4	225	2	BB214723	BB214723	BB214723
1007	75.8	2.4	699	6	CD628631	CD628631	56097494H
1008	75.2	2.4	234	2	BB327897	BB327897	BB327897
1009	75.2	2.4	464	2	BE263633	BE263633	601192057
1010	75.2	2.4	658	4	BG424478	BG424478	602447602
1011	75.2	2.4	715	5	BX849809	BX849809	BX849809
1012	75.2	2.4	865	5	BX844237	BX844237	BX844237
1013	75.2	2.4	917	5	BQ224963	BQ224963	AGENCOURT
1014	75	2.4	158	2	BB244145	BB244145	BB244145
1015	75	2.4	622	6	CA324358	CA324358	UI-M-FY0-
1016	75	2.4	1129	5	BQ071719	BQ071719	AGENCOURT
c1017	74.8	2.4	462	4	BF944916	BF944916	CM1-NN019
c1018	74.6	2.4	130	2	BE349795	BE349795	hq43b12.x
1019	74.6	2.4	789	4	BI686539	BI686539	603313631
c1020	74.4	2.4	228	1	AI323583	AI323583	mp57e06.x
1021	74.4	2.4	467	2	BF443467	BF443467	260957 MA
1022	74.4	2.4	661	7	CN333878	CN333878	170005315
1023	74.4	2.4	748	7	CF747865	CF747865	UI-M-HE0-
1024	74.4	2.4	763	7	CN461035	CN461035	UI-M-HB0-
1025	74	2.4	410	2	AW477508	AW477508	12794 MAR
1026	74	2.4	725	7	CN429210	CN429210	170004241
1027	74	2.4	771	7	CF285178	CF285178	AGENCOURT
1028	73.8	2.3	182	2	BB083305	BB083305	BB083305
1029	73.8	2.3	228	1	AV173854	AV173854	AV173854
1030	73.8	2.3	989	6	CA454865	CA454865	AGENCOURT
1031	73.6	2.3	414	6	CB801298	CB801298	AMGNNUC:M
1032	73.4	2.3	184	2	BB216676	BB216676	BB216676
1033	73.4	2.3	878	4	BM042998	BM042998	603619122
1034	73.4	2.3	1019	1	AL541401	AL541401	AL541401

1035	73.2	2.3	154	1	AV230195	AV230195	AV230195
1036	73.2	2.3	430	6	CB760771	CB760771	AMGNNUC:T
1037	73.2	2.3	580	7	CN333883	CN333883	170005318
1038	73	2.3	275	2	BB604391	BB604391	BB604391
c1039	73	2.3	526	5	BX267431	BX267431	BX267431
c1040	73	2.3	526	5	BX270851	BX270851	BX270851
c1041	73	2.3	528	5	BX270850	BX270850	BX270850
1042	73	2.3	716	7	CF747885	CF747885	UI-M-HE0-
1043	73	2.3	851	6	CD653925	CD653925	AGENCOURT
c1044	73	2.3	963	9	CC841964	CC841964	NDL.130G1
1045	73	2.3	3225	9	AY400492	AY400492	Pan trogl
c1046	72.8	2.3	355	6	CD631361	CD631361	56027755H
1047	72.8	2.3	569	6	CA352454	CA352454	623718 NC
1048	72.6	2.3	636	5	BQ109297	BQ109297	imageqc_6
c1049	72.6	2.3	820	1	AI800602	AI800602	wg12d10.x
1050	72.2	2.3	488	5	BQ044885	BQ044885	UI-M-EH0p
1051	72.2	2.3	539	7	CO051028	CO051028	Le_mx0_22
1052	72.2	2.3	843	7	CF995086	CF995086	AGENCOURT
1053	72.2	2.3	914	6	CA792253	CA792253	AGENCOURT
1054	71.8	2.3	228	2	BB213582	BB213582	BB213582
1055	71.4	2.3	680	6	BY735266	BY735266	BY735266
1056	71.4	2.3	715	6	CD628625	CD628625	56097386H
1057	71.4	2.3	3225	9	AY400491	AY400491	Homo sapi
1058	71.2	2.3	381	6	CB809999	CB809999	AMGNNUC:N
c1059	71.2	2.3	396	2	BE245837	BE245837	TCBAP1E19
1060	71.2	2.3	436	6	BY536630	BY536630	BY536630
1061	71.2	2.3	1005	5	BU553834	BU553834	AGENCOURT
1062	70.8	2.3	169	7	CK377833	CK377833	lai09b12.
1063	70.8	2.3	188	1	AV230685	AV230685	AV230685
1064	70.8	2.3	277	2	BB529518	BB529518	BB529518
1065	70.8	2.3	805	6	CD656935	CD656935	AGENCOURT
1066	70.6	2.2	767	9	CL640550	CL640550	G076F10 G
c1067	70.2	2.2	151	6	CB475278	CB475278	jns105_D0
1068	70.2	2.2	390	9	CL640447	CL640447	G074G07 G
c1069	70	2.2	228	1	AI837906	AI837906	UI-M-AL0-
1070	70	2.2	604	2	BE283742	BE283742	601103987
1071	70	2.2	777	7	CK479930	CK479930	AGENCOURT
1072	70	2.2	1911	9	AY403380	AY403380	Homo sapi
1073	69.8	2.2	163	7	CF424452	CF424452	lad30g10.
c1074	69.8	2.2	285	2	BF874390	BF874390	QV2-ET010
1075	69.6	2.2	157	2	BB151796	BB151796	BB151796
1076	69.6	2.2	266	7	Z28925	Z28925	HSBC1H081 S
1077	69.6	2.2	765	4	BI823626	BI823626	603038515
1078	69.6	2.2	832	7	CN534073	CN534073	UI-M-HO0-
1079	69.6	2.2	1154	4	BM462308	BM462308	AGENCOURT
1080	69.4	2.2	701	4	BI194321	BI194321	602947742
1081	69.2	2.2	343	5	BY173287	BY173287	BY173287
1082	69.2	2.2	555	1	AI641288	AI641288	fc13a11.y
1083	69	2.2	866	4	BG923853	BG923853	602824656
1084	69	2.2	894	4	BG422248	BG422248	602446883
1085	68.8	2.2	638	6	CD215884	CD215884	pgp2n.pk0
1086	68.8	2.2	641	7	CN665211	CN665211	A0823B11-
1087	68.8	2.2	728	6	CD628623	CD628623	56097378H
1088	68.6	2.2	695	5	BQ769222	BQ769222	UI-M-FC0-
c1089	68.4	2.2	325	2	BE246184	BE246184	TCBAP2E06
1090	68.4	2.2	518	6	BY593368	BY593368	BY593368
1091	68.2	2.2	439	1	AA263826	AA263826	LD07023.5

1092	68	2.2	786	1	AL584324	AL584324	AL584324
1093	67.8	2.2	243	7	CO187281	CO187281	EK027722.
1094	67.8	2.2	591	1	AL711630	AL711630	DKFZp686N
1095	67.8	2.2	626	7	CF535272	CF535272	UI-M-GH0-
1096	67.8	2.2	689	7	CN460658	CN460658	UI-M-HB0-
1097	67.8	2.2	849	7	CF726328	CF726328	UI-M-HB0-
1098	67.6	2.2	177	2	BB262424	BB262424	BB262424
1099	67.6	2.2	200	2	BB213365	BB213365	BB213365
1100	67.6	2.2	562	4	BM090629	BM090629	ig16e01.y
1101	67.6	2.2	582	5	BP215174	BP215174	BP215174
1102	67.6	2.2	768	6	CD619058	CD619058	56030577J
1103	67.6	2.2	4847	3	BC083186	BC083186	Mus muscu
1104	67.2	2.1	238	2	BB593587	BB593587	BB593587
1105	67.2	2.1	394	6	CB547006	CB547006	AMGNNUC:S
1106	67.2	2.1	692	7	CN236752	CN236752	RJB124H02
1107	67.2	2.1	3394	3	AK053632	AK053632	Mus muscu
1108	67	2.1	170	2	BB218573	BB218573	BB218573
1109	66.8	2.1	639	7	CV022901	CV022901	340 Full
c1110	66.8	2.1	710	1	AI638881	AI638881	tt08d08.x
1111	66.8	2.1	967	5	BX460723	BX460723	BX460723
1112	66.6	2.1	185	2	BB008412	BB008412	BB008412
1113	66.6	2.1	291	6	CB710224	CB710224	AMGNNUC:N
1114	66.6	2.1	813	6	CA320357	CA320357	UI-M-FW0-
1115	66.4	2.1	656	7	CF728356	CF728356	UI-M-HB0-
1116	66.4	2.1	777	7	CF742166	CF742166	UI-M-HB0-
1117	66.4	2.1	813	2	BE872958	BE872958	601451552
c1118	66.2	2.1	197	2	AW048928	AW048928	UI-M-BH1-
1119	66	2.1	639	6	CD502318	CD502318	CDA56-A04
1120	66	2.1	801	7	CK679212	CK679212	ZF101-P00
1121	65.6	2.1	668	7	CK836913	CK836913	4062174 B
1122	65.6	2.1	690	4	BG333712	BG333712	602460715
1123	65.4	2.1	264	2	BB532400	BB532400	BB532400
1124	65.4	2.1	580	5	BP326398	BP326398	BP326398
1125	65.2	2.1	343	5	BY351503	BY351503	BY351503
1126	65.2	2.1	731	7	CN458596	CN458596	UI-M-HB0-
1127	65.2	2.1	834	7	CF740100	CF740100	UI-M-HD0-
1128	65.2	2.1	1372	3	AK039355	AK039355	Mus muscu
1129	65	2.1	497	6	CA319520	CA319520	UI-M-FW0-
1130	65	2.1	701	6	BY736064	BY736064	BY736064
1131	64.8	2.1	278	2	BB523398	BB523398	BB523398
1132	64.8	2.1	597	7	CN255479	CN255479	170005322
1133	64.8	2.1	771	7	CK791448	CK791448	AGENCOURT
1134	64.6	2.1	320	5	BY346988	BY346988	BY346988
1135	64.2	2.0	346	5	BY018991	BY018991	BY018991
1136	64	2.0	147	1	AV315332	AV315332	AV315332
1137	64	2.0	576	7	CN333867	CN333867	170005318
1138	64	2.0	725	7	CN457302	CN457302	UI-M-HN0-
1139	64	2.0	757	7	CK635851	CK635851	UI-M-HN0-
1140	64	2.0	942	1	AU078986	AU078986	AU078986
1141	64	2.0	976	9	CNS02YCR	AL219492	Tetraodon
1142	64	2.0	1155	2	BF531775	BF531775	602072681
1143	63.8	2.0	591	4	BJ074142	BJ074142	BJ074142
1144	63.8	2.0	655	4	BJ063284	BJ063284	BJ063284
1145	63.8	2.0	723	4	BI870437	BI870437	603395690
1146	63.8	2.0	900	6	C82295	C82295	C82295 Leuk
1147	63.8	2.0	2319	9	AY402636	AY402636	Homo sapi
1148	63.8	2.0	2960	3	AK043634	AK043634	Mus muscu

1149	63.8	2.0	3154	3	AK033597	AK033597	Mus muscu
1150	63.8	2.0	3287	3	AK048364	AK048364	Mus muscu
1151	63.8	2.0	3292	3	AK037034	AK037034	Mus muscu
1152	63.8	2.0	3436	3	AK014333	AK014333	Mus muscu
1153	63.6	2.0	233	2	BB327844	BB327844	BB327844
1154	63.6	2.0	573	6	CD214656	CD214656	pgm2n.pk0
1155	63.6	2.0	831	7	CO433634	CO433634	UI-M-HX0-
1156	63.4	2.0	571	7	CN401141	CN401141	170006000
1157	63.4	2.0	676	6	CD803405	CD803405	UI-M-GV0-
1158	63.4	2.0	889	1	AU050267	AU050267	AU050267
1159	63.2	2.0	700	4	BI143486	BI143486	602907665
1160	63	2.0	232	2	BB169302	BB169302	BB169302
1161	63	2.0	370	5	BY028015	BY028015	BY028015
1162	62.8	2.0	1020	6	CB590629	CB590629	AGENCOURT
1163	62.6	2.0	214	2	BB269367	BB269367	BB269367
c1164	62.6	2.0	384	2	AW900477	AW900477	CM0-NN100
1165	62.6	2.0	469	7	CN429155	CN429155	170005318
1166	62.6	2.0	508	6	CD675182	CD675182	fs20a08.y
1167	62.6	2.0	602	5	BQ749127	BQ749127	UI-M-FD0-
1168	62.6	2.0	939	5	BU915658	BU915658	AGENCOURT
1169	62.4	2.0	150	1	AV237564	AV237564	AV237564
1170	62.4	2.0	555	7	CN670016	CN670016	A0887D08-
1171	62.4	2.0	2289	9	AY402637	AY402637	Pan trogl
1172	62.2	2.0	178	2	BB603730	BB603730	BB603730
1173	62.2	2.0	857	4	BI161471	BI161471	602865054
1174	62	2.0	857	2	BF580228	BF580228	602099043
1175	62	2.0	883	5	BU224821	BU224821	603948128
1176	61.8	2.0	469	1	AU279333	AU279333	AU279333
1177	61.8	2.0	685	1	AL637843	AL637843	AL637843
1178	61.8	2.0	856	7	CO246694	CO246694	AGENCOURT
1179	61.6	2.0	212	2	BB587253	BB587253	BB587253
c1180	61.6	2.0	580	7	CO302404	CO302404	EK184063.
1181	61.6	2.0	859	5	BQ571689	BQ571689	UI-M-FC0-
1182	61.4	2.0	155	2	BB222407	BB222407	BB222407
c1183	61.4	2.0	1056	9	CNS00JQN	AL076816	Drosophil
1184	61.2	1.9	170	2	BB113286	BB113286	BB113286
1185	61.2	1.9	490	7	CN538039	CN538039	UI-M-HS0-
1186	61.2	1.9	1084	4	BG479750	BG479750	602526948
1187	61	1.9	203	1	AA326134	AA326134	EST29247
c1188	61	1.9	398	1	AI787249	AI787249	uj58a10.x
1189	61	1.9	421	7	CN401145	CN401145	170004241
1190	60.8	1.9	441	6	CA871124	CA871124	K0908A03-
1191	60.8	1.9	1039	5	BX458912	BX458912	BX458912
1192	60.8	1.9	1170	2	BF345508	BF345508	602019266
1193	60.6	1.9	207	7	CN700205	CN700205	E0431G12-
1194	60.6	1.9	675	6	BY718955	BY718955	BY718955
1195	60.6	1.9	959	1	AL551337	AL551337	AL551337
c1196	60	1.9	395	4	BF947978	BF947978	CM1-NN019
c1197	60	1.9	587	6	CB585337	CB585337	AMGNNUC:U
1198	59.8	1.9	812	6	CA317902	CA317902	UI-M-FW0-
1199	59.6	1.9	403	7	CF535184	CF535184	UI-M-GI0-
1200	59.6	1.9	765	7	CK366996	CK366996	AGENCOURT
1201	59.4	1.9	546	2	BF194361	BF194361	246370 MA
1202	59.4	1.9	736	5	BM947302	BM947302	UI-M-EH0p
1203	59.2	1.9	986	4	BI686422	BI686422	603315567
1204	59	1.9	265	7	M78717	M78717	EST00865 Hi
c1205	59	1.9	373	4	BG998374	BG998374	PM4-HT130

1206	59	1.9	983	5	BQ879085	BQ879085	AGENCOURT
1207	59	1.9	2227	9	AY403445	AY403445	Mus muscu
1208	58.8	1.9	342	2	BE246502	BE246502	TCBAP1D47
c1209	58.8	1.9	595	5	BX672477	BX672477	BX672477
c1210	58.8	1.9	718	7	CK776486	CK776486	967641 MA
1211	58.8	1.9	814	2	BF348116	BF348116	602022006
1212	58.8	1.9	944	5	BQ931286	BQ931286	AGENCOURT
1213	58.6	1.9	338	2	BE246248	BE246248	TCBAP2D06
1214	58.6	1.9	456	4	BG015017	BG015017	PM1-GN018
1215	58.6	1.9	498	1	AA190645	AA190645	zq44a06.r
1216	58.6	1.9	628	6	CB577722	CB577722	AMGNNUC:N
1217	58.6	1.9	987	2	BE727277	BE727277	601560955
1218	58.4	1.9	581	5	BP198298	BP198298	BP198298
1219	58.4	1.9	595	1	AL678465	AL678465	AL678465
1220	58.4	1.9	599	1	AL678560	AL678560	AL678560
1221	58.4	1.9	766	4	BI335382	BI335382	602997946
1222	58.4	1.9	1109	4	BM547638	BM547638	AGENCOURT
1223	58.4	1.9	1121	4	BM477901	BM477901	AGENCOURT
1224	58.2	1.9	480	5	BY247585	BY247585	BY247585
1225	58.2	1.9	581	5	BP196129	BP196129	BP196129
1226	58.2	1.9	608	1	AI258757	AI258757	LP02029.5
1227	58.2	1.9	674	1	AU138132	AU138132	AU138132
1228	58.2	1.9	921	2	BF237200	BF237200	602028155
1229	57.8	1.8	148	1	AV378912	AV378912	AV378912
1230	57.8	1.8	173	2	AW983563	AW983563	RC3-HN000
1231	57.8	1.8	419	6	CB764881	CB764881	AMGNNUC:N
1232	57.8	1.8	634	6	CB548205	CB548205	AMGNNUC:C
1233	57.8	1.8	634	6	CB577061	CB577061	AMGNNUC:C
1234	57.8	1.8	840	6	CB990331	CB990331	AGENCOURT
1235	57.6	1.8	253	6	CA394719	CA394719	cs55b06.y
1236	57.6	1.8	554	4	BI683327	BI683327	464671 MA
1237	57.6	1.8	574	4	BJ068614	BJ068614	BJ068614
1238	57.6	1.8	631	6	CA876860	CA876860	K0951D08-
1239	57.6	1.8	703	4	BJ733929	BJ733929	BJ733929
1240	57.6	1.8	767	7	CO246012	CO246012	AGENCOURT
1241	57.6	1.8	911	5	BQ278955	BQ278955	AGENCOURT
1242	57.4	1.8	463	4	BI515157	BI515157	BB160017B
1243	57.4	1.8	611	5	BX852769	BX852769	BX852769
1244	57.4	1.8	755	4	BG326539	BG326539	602425385
1245	57.4	1.8	770	6	CA945576	CA945576	UI-M-FD0-
c1246	57.2	1.8	573	2	BE070335	BE070335	QV4-BT040
1247	57.2	1.8	690	1	AU134748	AU134748	AU134748
1248	57.2	1.8	698	5	BX344176	BX344176	BX344176
1249	57.2	1.8	811	7	CK482600	CK482600	AGENCOURT
1250	57.2	1.8	990	4	BI652258	BI652258	603299702
1251	57.2	1.8	1018	4	BI519944	BI519944	603071726
1252	57	1.8	444	6	BY531725	BY531725	BY531725
1253	57	1.8	533	4	BI499160	BI499160	ie27d02.y
1254	57	1.8	815	4	BI689717	BI689717	603316221
1255	57	1.8	945	7	CF579434	CF579434	AGENCOURT
1256	56.8	1.8	774	7	CN539668	CN539668	UI-M-HU0-
1257	56.8	1.8	884	2	BE728944	BE728944	601562382
1258	56.8	1.8	917	4	BI913405	BI913405	603179004
1259	56.6	1.8	148	2	BB225254	BB225254	BB225254
1260	56.6	1.8	618	7	CN429152	CN429152	170006000
1261	56.6	1.8	624	6	CB527987	CB527987	UI-M-FY0-
c1262	56.4	1.8	148	2	AW045210	AW045210	UI-M-BH1-

1263	56.4	1.8	561	1	AA929737	AA929737	vz05h07.r
c1264	56.4	1.8	576	2	BE831264	BE831264	PM2-MT004
1265	56.4	1.8	589	7	CF179045	CF179045	813129 MA
1266	56.4	1.8	907	7	CF583319	CF583319	AGENCOURT
c1267	56.2	1.8	117	2	BF470020	BF470020	UI-M-BH3-
1268	56.2	1.8	222	2	BB548578	BB548578	BB548578
1269	56.2	1.8	794	9	CL640418	CL640418	G074D03 G
1270	56	1.8	822	5	BU208115	BU208115	603952728
1271	55.8	1.8	656	6	CD628627	CD628627	56097394H
1272	55.8	1.8	670	1	AL870127	AL870127	AL870127
c1273	55.8	1.8	717	7	CK225357	CK225357	704281487
1274	55.8	1.8	1051	5	BQ898681	BQ898681	AGENCOURT
1275	55.6	1.8	510	1	AA823166	AA823166	vw41e06.r
1276	55.6	1.8	596	5	BP872160	BP872160	BP872160
1277	55.4	1.8	307	1	AA354547	AA354547	EST62826
1278	55.4	1.8	391	6	CB775786	CB775786	AMGNNUC:N
1279	55.4	1.8	575	7	CN685188	CN685188	E0204H04-
1280	55.4	1.8	599	5	BP218578	BP218578	BP218578
1281	55.4	1.8	637	1	AU135310	AU135310	AU135310
1282	55.2	1.8	258	1	AA601686	AA601686	no02b07.s
c1283	55.2	1.8	428	5	BX683168	BX683168	BX683168
1284	55.2	1.8	647	7	CK338348	CK338348	C0629B03-
1285	55.2	1.8	672	6	BY751398	BY751398	BY751398
1286	55.2	1.8	754	7	CN538762	CN538762	UI-M-HS0-
1287	55.2	1.8	1066	4	BG542239	BG542239	602571680
1288	55	1.7	469	4	BG348876	BG348876	de74a05.y
1289	55	1.7	546	9	CG594195	CG594195	OST252072
1290	54.6	1.7	683	5	BU269132	BU269132	603506561
1291	54.6	1.7	938	5	BU150466	BU150466	AGENCOURT
1292	54.4	1.7	486	2	BE982860	BE982860	UI-M-CG0p
1293	54.4	1.7	711	7	CK694093	CK694093	ZF101-P00
1294	54.4	1.7	745	5	BU345393	BU345393	603523405
c1295	54	1.7	195	1	AI030698	AI030698	UI-R-C0-j
1296	54	1.7	573	2	BF550969	BF550969	UI-R-C0-j
1297	54	1.7	598	6	CB434784	CB434784	611453 MA
1298	54	1.7	600	5	BU924827	BU924827	7102-54 M
1299	54	1.7	925	9	CNS0091P	AL053013	Drosophil
1300	54	1.7	1106	6	CD498549	CD498549	CDA34-C01
1301	53.8	1.7	347	7	CN335013	CN335013	170005360
1302	53.8	1.7	598	4	BI908590	BI908590	603069993
1303	53.8	1.7	731	7	CR769103	CR769103	DKFZp469L
1304	53.6	1.7	651	6	BY722642	BY722642	BY722642
1305	53.4	1.7	1075	5	BM918793	BM918793	AGENCOURT
c1306	53.4	1.7	1462	3	CR715185	CR715185	Tetraodon
1307	53.2	1.7	562	7	CO322494	CO322494	EK188241.
1308	53.2	1.7	595	1	AL876266	AL876266	AL876266
1309	53.2	1.7	785	7	CO428820	CO428820	UI-M-HX0-
1310	53.2	1.7	987	9	CNS00418	AL066537	Drosophil
1311	52.8	1.7	345	4	BG148558	BG148558	uu80g02.y
1312	52.8	1.7	488	2	BF773594	BF773594	283122 MA
c1313	52.8	1.7	519	6	CB435264	CB435264	615337 MA
1314	52.8	1.7	787	4	BG783400	BG783400	SEAUMC003
1315	52.8	1.7	809	5	BU232264	BU232264	603410226
1316	52.6	1.7	442	7	CK392174	CK392174	K0842D11-
c1317	52.6	1.7	493	4	BG009731	BG009731	QV1-GN031
1318	52.6	1.7	564	2	AW659026	AW659026	95939 MAR
1319	52.6	1.7	626	1	AU137591	AU137591	AU137591

c1320	52.6	1.7	760	5	BX919359	BX919359	BX919359
1321	52.6	1.7	787	5	BU610933	BU610933	UI-M-FC0-
1322	52.6	1.7	817	4	BG342624	BG342624	602374614
1323	52.6	1.7	870	5	BU612231	BU612231	UI-M-EW0-
1324	52.6	1.7	2307	9	AY407762	AY407762	Mus muscu
1325	52.4	1.7	428	4	BI882131	BI882131	fm85b03.x
1326	52.4	1.7	525	2	BE260428	BE260428	601150894
1327	52.4	1.7	621	4	BI066930	BI066930	pgfln.pk0
1328	52.4	1.7	688	2	BE385519	BE385519	601278033
1329	52.4	1.7	699	6	CA327319	CA327319	UI-M-FY0-
1330	52.4	1.7	704	4	BG829860	BG829860	602764154
1331	52.4	1.7	927	5	BU148244	BU148244	AGENCOURT
1332	52.4	1.7	938	4	BG830609	BG830609	602767211
1333	52.2	1.7	387	5	BY093485	BY093485	BY093485
1334	52.2	1.7	740	4	BG831840	BG831840	602765483
1335	52.2	1.7	938	4	BG422234	BG422234	602446867
1336	52.2	1.7	962	4	BG324610	BG324610	602422587
1337	52	1.7	391	4	BJ620346	BJ620346	BJ620346
1338	52	1.7	479	4	BG010829	BG010829	IL5-GN024
1339	52	1.7	814	7	CK476539	CK476539	AGENCOURT
1340	52	1.7	2411	6	CB605722	CB605722	AMGNNUC:M
1341	51.8	1.6	576	4	BI067451	BI067451	pgfln.pk0
1342	51.8	1.6	687	4	BI916243	BI916243	603178146
1343	51.8	1.6	751	6	CA317826	CA317826	UI-M-FW0-
1344	51.6	1.6	588	5	BP218616	BP218616	BP218616
1345	51.6	1.6	761	7	CO734982	CO734982	SLLE04c10
1346	51.6	1.6	835	7	CO733414	CO733414	SLLT02c05
c1347	51.4	1.6	73	6	CD631367	CD631367	56027839H
1348	51.4	1.6	321	7	CO291094	CO291094	EK076120.
1349	51.4	1.6	367	6	CD371550	CD371550	UI-R-GO0-
1350	51.4	1.6	533	5	BU484169	BU484169	603469842
1351	51.4	1.6	647	4	BI067436	BI067436	pgfln.pk0
1352	51.4	1.6	743	6	CA326974	CA326974	UI-M-FY0-
1353	51.4	1.6	802	5	BU613129	BU613129	UI-M-EW0-
1354	51.4	1.6	1929	9	AY403444	AY403444	Pan trogl
1355	51.2	1.6	397	6	CB772279	CB772279	AMGNNUC:M
1356	51.2	1.6	582	5	BP349308	BP349308	BP349308
c1357	51.2	1.6	659	1	AI651838	AI651838	wb55h11.x
1358	51.2	1.6	675	2	BF707801	BF707801	A379 LE A
1359	51.2	1.6	728	1	AU137554	AU137554	AU137554
1360	51.2	1.6	748	1	AU136052	AU136052	AU136052
1361	51.2	1.6	773	5	BU515916	BU515916	AGENCOURT
1362	51.2	1.6	925	4	BG324814	BG324814	602423928
1363	51.2	1.6	948	4	BG325041	BG325041	602423476
1364	51	1.6	478	7	CN290121	CN290121	170005319
1365	51	1.6	563	4	BI791273	BI791273	id03h12.y
1366	51	1.6	755	1	AU137539	AU137539	AU137539
1367	51	1.6	774	7	CN537492	CN537492	UI-M-HS0-
1368	51	1.6	804	7	CO430718	CO430718	UI-M-HX0-
1369	51	1.6	2227	9	AY403443	AY403443	Homo sapi
1370	51	1.6	2596	3	AK053115	AK053115	Mus muscu
1371	50.8	1.6	650	7	CR429569	CR429569	CR429569
1372	50.8	1.6	671	6	CD295461	CD295461	StrPu691.
1373	50.8	1.6	760	2	BF181876	BF181876	601805303
1374	50.4	1.6	604	4	BI183160	BI183160	UNL-P-FN-
1375	50.2	1.6	283	7	CF136469	CF136469	UI-HF-BN0
1376	50.2	1.6	475	9	CL212177	CL212177	G033C05 G

1377	50.2	1.6	836	7	CK600018	CK600018	AGENCOURT
1378	50	1.6	505	2	BE487489	BE487489	176253 BA
1379	50	1.6	701	6	CB245456	CB245456	UI-M-FY0-
1380	50	1.6	735	1	AU140116	AU140116	AU140116
1381	49.8	1.6	519	4	BM741971	BM741971	K-EST0014
1382	49.8	1.6	805	5	BX844812	BX844812	BX844812
1383	49.6	1.6	300	7	CN255485	CN255485	170004251
1384	49.6	1.6	410	6	CB803735	CB803735	AMGNNUC:N
1385	49.6	1.6	549	6	CB614718	CB614718	AMGNNUC:N
1386	49.6	1.6	580	5	BU432018	BU432018	603836176
1387	49.6	1.6	612	7	CN951333	CN951333	Ha_mx0_46
1388	49.6	1.6	773	4	BI218305	BI218305	602934473
1389	49.4	1.6	410	6	CB153520	CB153520	K-EST0210
c1390	49.4	1.6	423	4	BI058070	BI058070	PM4-GN050
1391	49.4	1.6	516	6	CD619063	CD619063	56053362H
1392	49.4	1.6	516	6	CD619065	CD619065	56053454H
c1393	49.4	1.6	538	6	CD619064	CD619064	56053362J
c1394	49.4	1.6	550	6	CD619062	CD619062	56053346J
c1395	49.4	1.6	551	6	CD619060	CD619060	56053340J
c1396	49.4	1.6	552	6	CD619066	CD619066	56053454J
1397	49.4	1.6	559	6	CA872840	CA872840	K0920H08-
1398	49.4	1.6	595	5	BP271999	BP271999	BP271999
1399	49.4	1.6	688	4	BI552143	BI552143	603195086
1400	49.4	1.6	749	9	CNS02V9F	AL215484	Tetraodon
1401	49.4	1.6	766	4	BG825242	BG825242	602747664
1402	49.4	1.6	771	4	BI859915	BI859915	603386049
1403	49.4	1.6	910	9	CNS033DR	AL226008	Tetraodon
1404	49.2	1.6	542	4	BM740534	BM740534	K-EST0011
1405	49.2	1.6	544	4	BM766233	BM766233	K-EST0048
1406	49.2	1.6	626	4	BM740685	BM740685	K-EST0012
c1407	49.2	1.6	897	9	CG766342	CG766342	TcB48.4_B
c1408	49.2	1.6	898	9	CG770102	CG770102	TcB51.2_A
c1409	49.2	1.6	901	5	BQ433090	BQ433090	AGENCOURT
1410	49.2	1.6	904	5	BQ735037	BQ735037	AGENCOURT
1411	49.2	1.6	1177	5	BM906470	BM906470	AGENCOURT
1412	49.2	1.6	1309	5	BU541920	BU541920	AGENCOURT
c1413	49	1.6	293	6	CD631363	CD631363	56027739H
c1414	49	1.6	695	7	CK225361	CK225361	704197850
1415	49	1.6	1161	3	CR679362	CR679362	Tetraodon
c1416	48.8	1.6	372	1	AA984436	AA984436	am86d04.s
1417	48.8	1.6	412	6	CB801382	CB801382	AMGNNUC:M
1418	48.8	1.6	473	8	AQ603447	AQ603447	HS_2126_A
1419	48.8	1.6	610	2	BB613257	BB613257	BB613257
1420	48.8	1.6	726	7	CN042616	CN042616	v11_p43_g
1421	48.6	1.5	431	6	CB757701	CB757701	AMGNNUC:M
1422	48.6	1.5	702	4	BI771035	BI771035	603055382
1423	48.6	1.5	1809	3	AK051165	AK051165	Mus muscu
1424	48.6	1.5	3317	3	AK052671	AK052671	Mus muscu
1425	48.6	1.5	3672	3	AK028900	AK028900	Mus muscu
1426	48.6	1.5	4248	3	AK031704	AK031704	Mus muscu
1427	48.4	1.5	416	5	BY224521	BY224521	BY224521
1428	48.4	1.5	539	1	AL918018	AL918018	AL918018
1429	48.2	1.5	428	6	CB794320	CB794320	AMGNNUC:N
1430	48.2	1.5	640	6	CA334086	CA334086	NISC_ls05
1431	48.2	1.5	876	6	CA489866	CA489866	AGENCOURT
1432	48	1.5	384	6	CB703233	CB703233	AMGNNUC:N
1433	48	1.5	569	4	BI775284	BI775284	467707 MA

1434	48	1.5	817	7	CF994909	CF994909	AGENCOURT
c1435	48	1.5	963	5	BX341410	BX341410	BX341410
1436	47.8	1.5	253	4	BF988853	BF988853	IL5-GN017
1437	47.8	1.5	254	4	BM030705	BM030705	495185 MA
1438	47.8	1.5	406	6	CB808351	CB808351	AMGNNUC:S
c1439	47.8	1.5	420	2	AW803853	AW803853	IL2-UM008
c1440	47.8	1.5	537	6	CB717637	CB717637	AMGNNUC:U
1441	47.8	1.5	633	7	CN295126	CN295126	170005326
1442	47.8	1.5	975	2	BF101157	BF101157	601754732
1443	47.6	1.5	619	4	BI648895	BI648895	603275856
1444	47.6	1.5	709	6	CD348531	CD348531	UI-M-FY0-
1445	47.6	1.5	777	5	BU708565	BU708565	UI-M-FI0-
c1446	47.6	1.5	796	1	AL561140	AL561140	AL561140
1447	47.6	1.5	1911	9	AY403382	AY403382	Mus muscu
c1448	47.4	1.5	240	4	BI000873	BI000873	MR3-HN006
c1449	47.4	1.5	469	1	AA859662	AA859662	UI-R-E0-b
1450	47.4	1.5	613	5	BX271575	BX271575	BX271575
1451	47.2	1.5	645	4	BI066459	BI066459	pgfln.pk0
1452	47.2	1.5	654	2	BB037994	BB037994	BB037994
c1453	47.2	1.5	737	9	CR018931	CR018931	Reverse s
1454	47.2	1.5	775	5	BU703431	BU703431	UI-M-FO0-
1455	47.2	1.5	1023	6	CD245257	CD245257	AGENCOURT
c1456	47	1.5	367	5	BQ320183	BQ320183	PM4-CT082
1457	47	1.5	480	7	CR579310	CR579310	CR579310
1458	47	1.5	511	4	BI673056	BI673056	ft33e03.y
1459	47	1.5	516	6	CD619061	CD619061	56053346H
1460	47	1.5	543	1	AA940432	AA940432	vz48h07.r
1461	47	1.5	625	4	BI753404	BI753404	603026593
1462	47	1.5	834	7	CF149484	CF149484	AGENCOURT
1463	46.8	1.5	350	5	BY200122	BY200122	BY200122
1464	46.8	1.5	365	2	AW437778	AW437778	79230 MAR
1465	46.8	1.5	635	1	AL852575	AL852575	AL852575
c1466	46.8	1.5	741	2	BF232471	BF232471	de06c04.x
1467	46.8	1.5	932	9	CNS022IX	AL178242	Tetraodon
1468	46.8	1.5	950	5	BU175283	BU175283	AGENCOURT
c1469	46.8	1.5	1131	5	BM922197	BM922197	AGENCOURT
1470	46.6	1.5	533	1	AA175711	AA175711	ms97a05.r
1471	46.6	1.5	609	4	BI066327	BI066327	pgfln.pk0
1472	46.6	1.5	641	6	BY728676	BY728676	BY728676
1473	46.6	1.5	688	4	BG700674	BG700674	602682306
1474	46.4	1.5	395	6	CB773879	CB773879	AMGNNUC:N
c1475	46.4	1.5	678	9	CC569313	CC569313	CH240_444
1476	46.4	1.5	957	4	BG261855	BG261855	602373655
1477	46.4	1.5	971	4	BG342228	BG342228	602374305
c1478	46.4	1.5	985	5	BX402983	BX402983	BX402983
1479	46.4	1.5	994	5	BQ929877	BQ929877	AGENCOURT
1480	46.2	1.5	564	7	CK635703	CK635703	UI-M-HN0-
1481	46.2	1.5	570	2	BE033028	BE033028	133242 MA
1482	46.2	1.5	590	9	AY420627	AY420627	Homo sapi
1483	46.2	1.5	594	7	CN409468	CN409468	170004276
1484	46.2	1.5	624	2	AW328571	AW328571	ds03d12.x
1485	46.2	1.5	634	5	BM951500	BM951500	UI-M-EG0-
1486	46.2	1.5	650	7	CF746951	CF746951	UI-M-HE0-
1487	46.2	1.5	658	7	CN409465	CN409465	170005325
1488	46.2	1.5	678	7	CN409457	CN409457	170004177
1489	46.2	1.5	732	7	CN409463	CN409463	170005325
1490	46.2	1.5	732	7	CN531114	CN531114	UI-M-HO0-

1491	46.2	1.5	741	7	CF730435	CF730435 UI-M-GZ0-
1492	46.2	1.5	778	7	CF736303	CF736303 UI-M-HD0-
1493	46	1.5	394	6	CB776561	CB776561 AMGNNUC:S
c1494	46	1.5	428	1	AI458053	AI458053 tj66h10.x
1495	46	1.5	528	2	BE334076	BE334076 us29e10.y
1496	46	1.5	575	5	BP338720	BP338720 BP338720
1497	46	1.5	714	7	CR789306	CR789306 DKFZp4590
1498	46	1.5	2775	3	AK077021	AK077021 Mus muscu
1499	45.8	1.5	372	2	BF443919	BF443919 261588 MA
1500	45.8	1.5	375	6	CB691762	CB691762 AMGNNUC:M

ALIGNMENTS

RESULT 1

CR623694

LOCUS CR623694 3005 bp mRNA linear HTC 21-JUL-2004

DEFINITION full-length cDNA clone CS0DL005YC17 of B cells (Ramos cell line)
Cot 25-normalized of Homo sapiens (human).

ACCESSION CR623694

VERSION CR623694.1 GI:50504501

KEYWORDS HTC; CNSLT_cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3005)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600
Faraday Avenue

REFERENCE 2 (bases 1 to 3005)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES Location/Qualifiers

source

1. .3005

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DL005YC17"

/tissue_type="B cells (Ramos cell line) Cot 25-normalized"

/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 95.6%; Score 3005; DB 3; Length 3005;
Best Local Similarity 100.0%; Pred. No. 0;

	Matches	3005;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	99	CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC	158							
Db	1	CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC	60							
Qy	159	TTCCAAGTGCCTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGGCC	218							
Db	61	TTCCAAGTGCCTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGGCC	120							
Qy	219	ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG	278							
Db	121	ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG	180							
Qy	279	AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG	338							
Db	181	AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG	240							
Qy	339	GGGGCTCGAGAAGCCATTCTGGCCTTGATATCCAGGATCCAGGGGTCCCAGGCTAAAG	398							
Db	241	GGGGCTCGAGAAGCCATTCTGGCCTTGATATCCAGGATCCAGGGGTCCCAGGCTAAAG	300							
Qy	399	AACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAG	458							
Db	301	AACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAG	360							
Qy	459	AGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAATGTCACCCAT	518							
Db	361	AGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAATGTCACCCAT	420							
Qy	519	CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGAT	578							
Db	421	CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGAT	480							
Qy	579	TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT	638							
Db	481	TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT	540							
Qy	639	GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG	698							
Db	541	GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG	600							
Qy	699	AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC	758							
Db	601	AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC	660							
Qy	759	AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT	818							
Db	661	AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT	720							
Qy	819	TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG	878							
Db	721	TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG	780							
Qy	879	AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG	938							
Db	781	AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG	840							

Qy	939	CTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAG	998
Db	841	CTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAG	900
Qy	999	CTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCC	1058
Db	901	CTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCC	960
Qy	1059	CACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTT	1118
Db	961	CACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTT	1020
Qy	1119	TGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAAC	1178
Db	1021	TGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAAC	1080
Qy	1179	AAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGT	1238
Db	1081	AAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGT	1140
Qy	1239	TGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATG	1298
Db	1141	TGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATG	1200
Qy	1299	GATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT	1358
Db	1201	GATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT	1260
Qy	1359	GCAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACC	1418
Db	1261	GCAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACC	1320
Qy	1419	ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA	1478
Db	1321	ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA	1380
Qy	1479	GAGATTACAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAG	1538
Db	1381	GAGATTACAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAG	1440
Qy	1539	GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAAGTGTAGT	1598
Db	1441	GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAAGTGTAGT	1500
Qy	1599	GTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCCGGGACCCCCACTGTGCCTGGGACCCT	1658
Db	1501	GTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCCGGGACCCCCACTGTGCCTGGGACCCT	1560
Qy	1659	GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATG	1718
Db	1561	GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATG	1620
Qy	1719	GAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT	1778
Db	1621	GAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT	1680

Qy	1779	CAGAGCCGCCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTC	1838
Db	1681	CAGAGCCGCCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTC	1740
Qy	1839	CCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTC	1898
Db	1741	CCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTC	1800
Qy	1899	CCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTT	1958
Db	1801	CCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTT	1860
Qy	1959	GGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTAC	2018
Db	1861	GGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTAC	1920
Qy	2019	TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGG	2078
Db	1921	TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGG	1980
Qy	2079	GAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAG	2138
Db	1981	GAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAG	2040
Qy	2139	TCCTACTGGCCCCACTTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCC	2198
Db	2041	TCCTACTGGCCCCACTTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCC	2100
Qy	2199	CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGC	2258
Db	2101	CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGC	2160
Qy	2259	TGTGAGACCCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCT	2318
Db	2161	TGTGAGACCCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCT	2220
Qy	2319	CCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACT	2378
Db	2221	CCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACT	2280
Qy	2379	GAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGG	2438
Db	2281	GAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGG	2340
Qy	2439	CTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTC	2498
Db	2341	CTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTC	2400
Qy	2499	CCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAG	2558
Db	2401	CCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAG	2460
Qy	2559	CAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGG	2618
Db	2461	CAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGG	2520
Qy	2619	GGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGT	2678

Db	2521	GGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGT	2580
Qy	2679	TCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTCAGAGACCCTAAAAAACCTGC	2738
Db	2581	TCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTCAGAGACCCTAAAAAACCTGC	2640
Qy	2739	CTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGC	2798
Db	2641	CTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGC	2700
Qy	2799	CACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAG	2858
Db	2701	CACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAG	2760
Qy	2859	GGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCA	2918
Db	2761	GGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCA	2820
Qy	2919	GGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAGTTGGGGCAGACTCTGAT	2978
Db	2821	GGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAGTTGGGGCAGACTCTGAT	2880
Qy	2979	CCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAG	3038
Db	2881	CCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAG	2940
Qy	3039	CTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTTCAGAAAACCTGCTTG	3098
Db	2941	CTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTTCAGAAAACCTGCTTG	3000
Qy	3099	TCAGA	3103
Db	3001	TCAGA	3005

RESULT 2

HSM807023

LOCUS HSM807023 3151 bp mRNA linear HTC 22-SEP-2004

DEFINITION Homo sapiens mRNA; cDNA DKFZp686D04248 (from clone DKFZp686D04248).

ACCESSION BX640891

VERSION BX640891.1 GI:34365195

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3151)

AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

CONSRM The German cDNA Consortium

TITLE Direct Submission

JOURNAL Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

Qy	322	GAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAG	381
Db	320	GAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAG	379
Qy	382	GGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAAT	441
Db	380	GGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAAT	439
Qy	442	GTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTT	501
Db	440	GTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTT	499
Qy	502	CTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCT	561
Db	500	CTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCT	559
Qy	562	TCATTGAAC TTCAAGATT CCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAA	621
Db	560	TCATTGAAC TTCAAGATT CCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAA	619
Qy	622	AAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGC	681
Db	620	AAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGC	679
Qy	682	TCTATTCTGGTACTATGAACAAC TTCTGAGGAGTGGCCATCCTGATGCGCACACTGG	741
Db	680	TCTATTCTGGTACTATGAACAAC TTCTGAGGAGTGGCCATCCTGATGCGCACACTGG	739
Qy	742	GATCCCAGCCTGTCTCAAGACCGACAAC TTCTCCGCTGGCTGCATCATGACGCCTCCT	801
Db	740	GATCCCAGCCTGTCTCAAGACCGACAAC TTCTCCGCTGGCTGCATCATGACGCCTCCT	799
Qy	802	TTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCG	861
Db	800	TTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCG	859
Qy	862	AGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACG	921
Db	860	AGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACG	919
Qy	922	TGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCT	981
Db	920	TGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCT	979
Qy	982	GCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCG	1041
Db	980	GCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCG	1039
Qy	1042	ATTCTCCACAGCTCCCCACATCTACGCAGTCTTACCTCCAGTGGCAGGTTGGCGGGA	1101
Db	1040	ATTCTCCACAGCTCCCCACATCTACGCAGTCTTACCTCCAGTGGCAGGTTGGCGGGA	1099
Qy	1102	CCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGA	1161
Db	1100	CCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGA	1159
Qy	1162	AATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCA	1221

Db	1160	 AATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCA	1219
Qy	1222	ACCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGA	1281
Db	1220	 ACCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGA	1279
Qy	1282	AGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCG	1341
Db	1280	 AGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCG	1339
Qy	1342	TGGAGTATACACGGCTTGCACTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTG	1401
Db	1340	 TGGAGTATACACGGCTTGCACTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTG	1399
Qy	1402	TCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCA	1461
Db	1400	 TCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCA	1459
Qy	1462	GTGCTCATCTGGTGGAAGAGATTAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGC	1521
Db	1460	 GTGCTCATCTGGTGGAAGAGATTAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGC	1519
Qy	1522	AGCTGGCCCCCACCAGGGTGCAGTGTGTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGC	1581
Db	1520	 AGCTGGCCCCCACCAGGGTGCAGTGTGTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGC	1579
Qy	1582	CCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGTCTGCCCCGACCCCC	1641
Db	1580	 CCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGTCTGCCCCGACCCCC	1639
Qy	1642	ACTGTGCCTGGGACCCAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACT	1701
Db	1640	 ACTGTGCCTGGGACCCAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACT	1699
Qy	1702	CCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGA	1761
Db	1700	 CCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGA	1759
Qy	1762	GCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCA	1821
Db	1760	 GCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCTA	1819
Qy	1822	ACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTC	1881
Db	1820	 ACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTC	1879
Qy	1882	ATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGA	1941
Db	1880	 ATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGA	1939
Qy	1942	TAGTGCAGGATGGAGTTGGGGGTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCAT	2001
Db	1940	 TAGTGCAGGATGGAGTTGGGGGTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCAT	1999
Qy	2002	ACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAAC	2061

Db	2000	ACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAAC	2059
Qy	2062	TGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCG	2121
Db	2060	TGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCG	2119
Qy	2122	CCCTGGCTGCCCAGCAGTCCCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCT	2181
Db	2120	CCCTGGCTGCCCAGCAGTCCCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCT	2179
Qy	2182	TAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTC	2241
Db	2180	TAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTC	2239
Qy	2242	GGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAG	2301
Db	2240	GGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAG	2299
Qy	2302	AGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACA	2361
Db	2300	AGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACA	2359
Qy	2362	ACAACCTGCCCTAGGCACCTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAG	2421
Db	2360	ACAACCTGCCCTAGGCACCTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAG	2419
Qy	2422	GCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCAC	2481
Db	2420	GCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCAC	2479
Qy	2482	AAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTC	2541
Db	2480	AAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTC	2539
Qy	2542	AGCAGGGTGATGCACAGCAGTCTGCCTCCCCATGCGGACTCCCTTCTACCAAGCACATGA	2601
Db	2540	AGCAGGGTGATGCACAGCAGTCTGCCTCCCCATGCGGACTCCCTTCTACCAAGCACATGA	2599
Qy	2602	GCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCT	2661
Db	2600	GCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCT	2659
Qy	2662	GGAGAGGATCCTTTCAGTTCTGGCCATTCCAGGGACCCCTCCAGAAACACAGTGTTTCAAGA	2721
Db	2660	GGAGAGGATCCTTTCAGTTCTGGCCATTCCAGGGACCCCTCCAGAAACACAGTGTTTCAAGA	2719
Qy	2722	GACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACA	2781
Db	2720	GACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACA	2779
Qy	2782	ATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCA	2841
Db	2780	ATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCA	2839
Qy	2842	ACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCG	2901
Db	2840	ACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCG	2899

Qy 2902 TGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAG 2961
 |||
 Db 2900 TGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAG 2959
 Qy 2962 TTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCT 3021
 |||
 Db 2960 TTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCT 3019
 Qy 3022 TCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGG 3081
 |||
 Db 3020 TCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGG 3079
 Qy 3082 ATTCAGAAACTGCTTGTCTCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAA 3141
 |||
 Db 3080 ATTCAGAAACTGCTTGTCTCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAA 3139
 Qy 3142 AA 3143
 ||
 Db 3140 AA 3141

RESULT 3

AY402621

LOCUS AY402621 2172 bp DNA linear GSS 12-DEC-2003

DEFINITION Homo sapiens HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY402621

VERSION AY402621.1 GI:39758607

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2172)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2172)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .2172
 /organism="Homo sapiens"
 /mol_type="genomic DNA"

```

gene          /db_xref="taxon:9606"
              <1..>2172
              /locus_tag="HCM1285"
ORIGIN
Query Match          59.6%;  Score 1874;  DB 9;  Length 2172;
Best Local Similarity 86.3%;  Pred. No. 0;
Matches 1874;  Conservative 0;  Mismatches 298;  Indels 0;  Gaps 0;

Qy      105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1   ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 60

Qy      165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 224
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 120

Qy      225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy      285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 240

Qy      345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 404
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 300

Qy      405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy      465 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 420

Qy      525 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTTAC 584
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTTAC 480

Qy      585 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCCTTTGACCCC 644
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCCTTTGACCCC 540

Qy      645 GCTCACAAGCATAACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCTCACAAGCATAACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 600

Qy      705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 764
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 660

Qy      765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
        ||||||||||||||||||||||||
Db      661 GACAACTTCCTCCGCTGGCTGCATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720

```

Qy	825	CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGGCTC	884
Db	721	NN	780
Qy	885	CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCAGAAAAGCTGCTGCAG	944
Db	781	NN	840
Qy	945	AAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC	1004
Db	841	NN	900
Qy	1005	TTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC	1064
Db	901	NN	960
Qy	1065	TACGCAGTCTTCACCTCCAGTGCGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTG TGCC 	1124
Db	961	NNNNNNNNNNNNNNNNNNNNNNNNGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTG TGCC	1020
Qy	1125	TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA 	1184
Db	1021	TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA	1080
Qy	1185	ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA 	1244
Db	1081	ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA	1140
Qy	1245	GTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG 	1304
Db	1141	GTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG	1200
Qy	1305	CAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTG CAGTG 	1364
Db	1201	CAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTG CAGTG	1260
Qy	1365	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA 	1424
Db	1261	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA	1320
Qy	1425	GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT 	1484
Db	1321	GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT	1380
Qy	1485	CAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGCCCCCACCCAGGGTGCA 	1544
Db	1381	CAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGCCCCCACCCAGGGTGCA	1440
Qy	1545	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTAT 	1604
Db	1441	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTAT	1500
Qy	1605	GAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC 	1664
Db	1501	GAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC	1560
Qy	1665	CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG	1724

Db	1561	CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACCTCTGGAAGCAGGACATGGAGCGG	1620
Qy	1725	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1784
Db	1621	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1680
Qy	1785	CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1844
Db	1681	CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1740
Qy	1845	CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1904
Db	1741	CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1800
Qy	1905	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1964
Db	1801	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1860
Qy	1965	CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	2024
Db	1861	CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	1920
Qy	2025	GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACCTGGCAGGCATCCCCGGGAGCAT	2084
Db	1921	GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACCTGGCAGGCATCCCCGGGAGCAT	1980
Qy	2085	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTAC	2144
Db	1981	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTAC	2040
Qy	2145	TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC	2204
Db	2041	TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC	2100
Qy	2205	ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG	2264
Db	2101	ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG	2160
Qy	2265	ACCCTGCGCCCT	2276
Db	2161	ACCCTGCGCCCT	2172

RESULT 4

AY402622

LOCUS AY402622 2133 bp DNA linear GSS 12-DEC-2003

DEFINITION Pan troglodytes HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY402622

VERSION AY402622.1 GI:39758608

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 2133)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2133)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .2133

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

gene <1. .>2133

/locus_tag="HCM1285"

ORIGIN

Query Match 56.2%; Score 1765.4; DB 9; Length 2133;

Best Local Similarity 82.9%; Pred. No. 0;

Matches 1769; Conservative 0; Mismatches 364; Indels 0; Gaps 0;

Qy 105 ATGGCCCTCCCAGCCCTGGGCCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164

Db 1 ATGGCCCTCCCAGCCCTGGGCCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 60

Qy 165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 224

Db 61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGANNCGGGCAGGGGCCCATGCCC 120

Qy 225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284

Db 121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy 285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344

Db 181 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 240

Qy 345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATG 404

Db 241 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATG 300

Qy 405 ATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464

Db 301 ATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy 465 GAGACACAGTGTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524

[illegible]

Qy	1365	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA	1424
Db	1261	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA	1320
Qy	1425	GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCCTCATCTGGTGGAAGAGATT	1484
Db	1321	GGGTCGNTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCCTCATCTGGTGGAANNNNNTT	1380
Qy	1485	CAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCA	1544
Db	1381	CAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCA	1440
Qy	1545	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTAT	1604
Db	1441	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTAT	1500
Qy	1605	GAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC	1664
Db	1501	GAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGCCTGGGATCCTGAGTCC	1560
Qy	1665	CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG	1724
Db	1561	CGAACCTGTTGCCTCCTNNNNNNNNNNNNNNNGAACTCCTGGAAGCAGGACATGGAGCGG	1620
Qy	1725	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1784
Db	1621	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1680
Qy	1785	CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1844
Db	1681	CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGAGNTCCCCTGC	1740
Qy	1845	CCCCACCTGTCAGCCTTGCCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1904
Db	1741	CCCCACCTGTCAGCCTTGCCCTCTTACTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1800
Qy	1905	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1964
Db	1801	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1860
Qy	1965	CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	2024
Db	1861	CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	1920
Qy	2025	GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT	2084
Db	1921	GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT	1980
Qy	2085	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCCTAC	2144
Db	1981	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCCTAC	2040
Qy	2145	TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATC	2204
Db	2041	TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATC	2100

Qy 2205 ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGG 2237
 ||||| | ||||||||| | |||||||||
Db 2101 ATCCTCNTGGCCTCCCCANNGAGAGCACTCCGG 2133

RESULT 5

AK077976

LOCUS	AK077976	3206 bp	mRNA	linear	HTC 03-APR-2004
-------	----------	---------	------	--------	-----------------

DEFINITION Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030492A12 product:sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A, full insert sequence.

ACCESSION AK077976

VERSION AK077976.1 GI:26097602

KEYWORDS HTC; CAP trapper.

SOURCE *Mus musculus* (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
-------	---

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3206)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.

FEATURES

source Location/Qualifiers

1. .3206

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM_DB:6030492A12"

/db_xref="taxon:10090"

/clone="6030492A12"

/sex="male"

/tissue_type="testis"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="13 days embryo"

misc_feature 224. .2507

/note="putative

sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A (MGD|MGI:107560, GB|NM_013658, evidence: BLASTN, 99%, match=2517) "

polyA_signal 3181. .3186

/note="putative"

polyA_site 3206

/note="putative"

ORIGIN

Query Match 55.6%; Score 1747.4; DB 3; Length 3206;

Best Local Similarity 76.7%; Pred. No. 0;

Matches 2355; Conservative 0; Mismatches 621; Indels 95; Gaps 14;

Qy 75 GAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCC 134
 || | ||||| || | ||||| ||||| ||| ||||| |||||
 Db 194 GAACCATCTGGTGACCATCTCAGGCTGACCATGGCCCTACCATCCCTGGGCCAGGACTCA 253

Qy 135 TGGAGCCTCCTGGGCCTTTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACC 194
 ||||| ||||| | |||| | ||||| || | |||| | | | |
 Db 254 TGGAGTCTCCTGCGTGTTTTTTTCTTCCAACCTCTTCTGCTGCCATCACTGCCACCTGCT 313

Qy 195 GCGGGGGGAGGCGGGCAGGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGT 254
 | ||| || | ||||| ||||| ||||| ||||| ||||| |||||
 Db 314 TCTGGGACTGGTGGTCAGGGGGCCCATGCCCAGAGTCAAATACCATGCTGGAGACGGGCAC 373

Qy 255 AGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGT 314
 ||||| || ||||| || || ||||| || ||||| ||||| |||||
 Db 374 AGGGCCCTCAGCTTCTTCCAACAAAAGGGCCTCCGAGACTTTGACACGCTGCTCCTGAGT 433

Qy 315 GGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAG 374
 | |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 434 GACGATGGCAACACTCTCTATGTGGGGGCTCGAGAGGCCGTCTGGCCTTGAATATCCAG 493

Qy 375 GATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAG 434
 | |||| | |||| | ||||| ||||| ||||| ||||| ||||| |||||
 Db 494 AATCCAGGAATCCCAAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGAGAGAAAAAAG 553

Qy 435 AGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTC 494
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 554 ACCGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATTGAGTC 613

Qy 495 CTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCT 554
 ||||| ||||| || || |||| | |||| | |||| | ||||| |||||
 Db 614 CTGGTCTCTTACAATGCTACTCACCTCTATGCCTGTGGGACCTTTGCCTTCAGCCCTGCC 673

Qy 555 TGTACCTTCATTGAACTTCAAGATTCCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATG 614
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 674 TGTACCTTCATTGAACTCCAAGATTCCCTCCTGTTGCCCATCTTGATAGACAAGGTCATG 733

Qy 615 GAGGGAAAAGGCCAAAGCCCCTTTGACCCGCTCACAAGCATACGGCTGTCTTGGTGGAT 674
 || || | ||||| ||||| ||||| | ||||| || ||||| |||||
 Db 734 GACGGGAAGGGCCAAAGCCCCTTTGACCTGTTCACAAGCACACAGCTGTCTTGGTTCGAT 793

Qy 675 GGGATGCTCTATTCTGGTACTATGAACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGC 734
 ||||| |||| | || || ||||| ||||| ||||| ||||| |||||
 Db 794 GGGATGCTTTATTCCGGCACCATGAACAACCTCCTGGGCAGCGAGCCCATCCTGATGCGG 853

Qy 735 AACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTCCTCCGCTGGCTGCATCATGAC 794
 ||||| ||||| ||||| |||| | |||| | ||||| ||||| ||
 Db 854 AACTGGGATCCCAGCCTGTTCTCAAGACTGACATCTTCTTACGCTGGCTGCACGCGGAT 913

Qy 795 GCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACA 854
 ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
 Db 914 GCCTCCTTCGTGGCAGCCATTCCATCCACCAGGTCGTCTATTTCTTCTTTGAGGAGACA 973

Qy 855 GCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAG 914
 ||||| ||||| ||||| || || | |||| | ||||| |||||
 Db 974 GCCAGCGAGTTTGACTTCTTTGAAGAGCTGTATATATCCAGGGTGGCTCAAGTCTGCAAG 1033

Qy 915 AATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCTGAAGGCCAG 974

Db	1034	AACGACGTGGGCGGTGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCTTCAAAGCCCAG	1093
Qy	975	CTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGTCTC	1034
Db	1094	TTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCCGCCACGCGGTCTGTCTG	1153
Qy	1035	CCCCCGGATTCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTT	1094
Db	1154	CCCCCGGATTCTCCCTCTGTTTCCCGCATCTACGCAGTCTTTACCTCCCAGTGGCAGGTT	1213
Qy	1095	GGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTT	1154
Db	1214	GGCGGGACCAGGAGCTCAGCAGTCTGTGCCTTCTCTCTCACGGACATTGAGCGAGTCTTT	1273
Qy	1155	AAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCT	1214
Db	1274	AAAGGGAGTACAAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACTTACCGGGGCTCA	1333
Qy	1215	GAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACC	1274
Db	1334	GAGGTCAGCCCGAGGCAAGGCAGTTGCTCCATGGGCCCCCTCCTCTGACAAAGCCTTGACC	1393
Qy	1275	TTCATGAAGGACCATTTCTCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAA	1334
Db	1394	TTCATGAAGGACCATTTTCTGATGGATGAGCACGTGGTAGGAACACCCCTGCTGGTGAAAG	1453
Qy	1335	TCTGGCGTGGAGTATACACGGCTTGCACTGGAGACAGCCAGGGCCTTGATGGGCACAGC	1394
Db	1454	TCTGGTGTGGAGTACACACGGCTTGCTGTGGAGTCAGCTCGGGGCCTTGATGGGAGCAGC	1513
Qy	1395	CATCTTGTTCATGTACCTGGGAACCACCACAGGTCGCTCCACAAGGCTGTGGTAAGTGGG	1454
Db	1514	CATGTGGTTCATGTATCTGGGTACCTCCACGGGTCCCTGCACAAGGCTGTGGTGCCTCAG	1573
Qy	1455	GACAGCAGTGCTCATCTGGTGGAAGAGATTGAGCTG-TTCCCTGACCCTGAACCTGTTTCG	1513
Db	1574	GACAGCAGTGCTTATCTCGTGGAGGAGATTGAGCTGAGCCCTGACTCTGAGCCTGTTTCG	1633
Qy	1514	CAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTG	1573
Db	1634	AAACCTGCAGCTGGCCCCCGCCAGGGTGCAGTGTTTGCAGGCTTCTCTGGAGGCATCTG	1693
Qy	1574	GAGGGTGGCCCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCG	1633
Db	1694	GAGAGTTCCAGGGCCAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCTTGGCAG	1753
Qy	1634	GGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAA	1693
Db	1754	GGACCCTCACTGTGCCTGGGACCCTGAATCAAGACTCTGCAGCCTTCTGTCTGGCTCTAC	1813
Qy	1694	CCTGAACCTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGG	1753
Db	1814	C---AAGCCTTGGAAGCAGGACATGGAACGCGGCAACCCGGAGTGGGTATGCACCCGTGG	1870
Qy	1754	CCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCTGGC	1813

Db 1871 CCCCATGGCCAGGAGCCCCCGGCGTCAGAGCCCCCTCAACTAATTAAAGAAGTCCTGAC 1930

Qy 1814 TGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTA 1873
 |||||

Db 1931 AGTCCCCAACTCCATCCTGGAGCTGCCCTGCCCCACCTGTCAGCACTGGCCTCTTACCA 1990

Qy 1874 TTGGAGTCATGGCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCT 1933
 |||||

Db 1991 CTGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGCTACCGTCTACAATGGCTCCCT 2050

Qy 1934 CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGTGGGCAACTGAGAATGG 1993
 |||||

Db 2051 CTTGCTGCTGCCGAGGATGGTGTGGAGGCCCTACCAGTGTGTGGCGACTGAGAACGG 2110

Qy 1994 CTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGA 2053
 ||

Db 2111 CTACTCATACCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCAGCCCCCTGGCGCTGGA 2170

Qy 2054 TCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCACTGG 2113
 |||||

Db 2171 CCCTGAGCTGGCGGGCGTTCCTCGTGAGCGTGTGCAGGTCCCGCTGACCAGGGTCGGAGG 2230

Qy 2114 TGGGGCCGCCCTGGCTGCCCAGCAGTCCCTACTGGCCCCACTTTGTCACTGTCACTGTCT 2173
 ||

Db 2231 CGGAGCTTCCATGGCTGCCCAGCGGTCCCTACTGGCCCCATTTTCTCATCGTTACCGTCT 2290

Qy 2174 CTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACT 2233
 ||

Db 2291 CCTGGCCATCGTGCTCCTGGGAGTGCTCACTCTCCTCCTCGCTTCCCCACTGGGGGCGCT 2350

Qy 2234 CCGGGCTCGGGGCAAGGTTCAAGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTT 2293
 |||||

Db 2351 GCGGGCTCGGGGTAAGGTTCAAGGCTGTGGGATGCTGCCCCCAGGGAAAAGGCTCCACT 2410

Qy 2294 AAGCAGAGAGCAACACCTCCAGTCTCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGA 2353
 |||||

Db 2411 GAGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGACGTAGA 2470

Qy 2354 CGCTGACAACAACCTGCCTAGGCAGTGAAGTAGCTTAAACTCTAGGCACAGGCCGGGGCT- 2412
 ||

Db 2471 TGCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACAGGGACACAGATCCGCAGCTG 2530

Qy 2413 -GCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCCAAGCACAGCCCTGACTAGGATG 2471
 ||

Db 2531 AGCAGAGCAAGCCACTGGCCTTGTTGGCTATGC----- 2563

Qy 2472 ACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACT 2531
 |||

Db 2564 ----CAGGCACAGTGCCACTCTGACCAGGGTAGGAGGCTCTCCTGCTAACGTGTGTACC 2619

Qy 2532 GATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACC 2591
 |

Db 2620 TACAGCACCCAGTAGG-----TCCTCCCCTGTGGGACTCTCTTCTGCA 2662

Qy 2592 AAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATAT 2651
 |

Db 2663 AGCACATTGGGCTGTCT-----CCATACCTGTACTTGTGCTGTGAC 2703

Qy 2652 TGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAG 2711
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2704 AGGAAGAGCCAGACAGGTTTCTTTGATTTTGATTGACCCAAGAGCCCTCCTGTAACAAAC 2763
 Qy 2712 TGTTTCAAGAGACCCTAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAA 2771
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2764 GTGCTCCAGGAGACCATGAAAGGTGTGGCTGTCTGGGATTCTGTGGTGACAAAC-CTAAG 2822
 Qy 2772 CATCTAAACAATCATATGCTA-----ACATGCCACTCCTGGAAACTCCACTCT----G 2820
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2823 CATCCGAGCAAGCTGGGGCTATTCTTGCAAACCTCCATCCTGAACGCTGTCACTCTAGAAG 2882
 Qy 2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAGGGATCTGCTCC 2879
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2883 CAGCTGCTGCTTTGAACACCAGCCCACCCTCCTTCCCAAGAGTCTCTATGGAGTTGGCCC 2942
 Qy 2880 CTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTG 2939
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2943 CTTGTGTTTCCTTTACCAGTCATGCCATACTGTTT---GGGAAGTCATCTCTGAAGTCTA 2999
 Qy 2940 ACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCT---TCTGCCCTGGC-AG 2995
 | | | | | | | | | | | | | | | | | | | | | |
 Db 3000 ACCACCTTCCTTCTTGCTTCAGTTTGGACAGATTGTTATTATTGTCTCTGCCCTGGCTAG 3059
 Qy 2996 AATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCT 3055
 | | | | | | | | | | | | | | | | | | | | | |
 Db 3060 AATGGGGGGCATAATCTGAGCCTTGTTCCTTGTCCAGTGTGGCTGACCCTTGACCTCTT 3119
 Qy 3056 CCCCCTCCCTTTTCCTTTGTTTTGGGATTTCAGAAACTGCTTGTGAGAGACTGTTTATTT 3115
 | | | | | | | | | | | | | | | | | | | | | |
 Db 3120 --CCTTCCTCCTCCCTTTGTTTTGGGATTTCAGAAACTGCTTGTGACAGACAATTTATTT 3177
 Qy 3116 TTTATTAAAAA 3126
 | | | | | | | | | | | | | | | | | | | | | |
 Db 3178 TTTATTAAAAA 3188

RESULT 6

AK035918

LOCUS AK035918 3086 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630018D15 product:sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A, full insert sequence.

ACCESSION AK035918

VERSION AK035918.1 GI:26084904

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636
 REFERENCE 2
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 3086)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL:<http://genome.gsc.riken.jp/>

URL:<http://fantom.gsc.riken.jp/>.

FEATURES
source Location/Qualifiers
1. .3086
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:9630018D15"
/db_xref="taxon:10090"
/clone="9630018D15"
/tissue_type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="16 days neonate"
misc_feature 59. .2388
/note="putative
sema domain, immunoglobulin domain (Ig), transmembrane
domain (TM) and short cytoplasmic domain, (semaphorin) 4A
(MGD|MGI:107560, GB|NM_013658, evidence: BLASTN, 99%,
match=2517)"
polyA_signal 3062. .3067
/note="putative"
polyA_site 3086
/note="putative"

ORIGIN

Query Match 54.1%; Score 1701.4; DB 3; Length 3086;
Best Local Similarity 75.2%; Pred. No. 0;
Matches 2364; Conservative 0; Mismatches 637; Indels 141; Gaps 14;

```
Qy      50 AACGCAGCGGCATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGC 109
      ||| |||      ||      | |||| | ||||| ||| ||||| |||||
Db       4 AATCCAGAAAGTGCCTGTTTCCTCAGAACCATCTGGTGACCATCTCAGGCTGACCATGGC 63

Qy     110 CCTCCCAGCCCTGGGCCCTGGACCCCTGGAGCCTCCTGGGCCCTTTTCTCTTCCAACCTGCT 169
      ||| ||| ||||| ||||| |||| | ||||| ||||| | ||| ||||| |||||
Db       64 CCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTTTTTTCTTCCAACCTCTT 123

Qy     170 TCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCAGGGT 229
      | |||||      | | | | | ||| || || ||||| ||||| ||||| ||
Db      124 CTGCTGCCATCACTGCCACCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCCAGAGT 183

Qy     230 CAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCA 289
      || |||| |||| || || | | |||| || ||||| ||||| || || |||||
Db     184 CAAATACCATGCTGGAGACGGGCACAGGGCCCTCAGCTTCTTCCAACAAAAAGGCCTCCG 243

Qy     290 GGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGA 349
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     244 AGACTTTGACACGCTGCTCCTGAGTGACGATGGCAACACTCTCTATGTGGGGGCTCGAGA 303

Qy     350 AGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACC 409
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     304 GGCCGTCTGGCCTTGAATATCCAGAACCCAGGAATCCCAAGGCTAAAGAACATGATACC 363

Qy     410 GTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCCTTTAAGAAGAAGAGCAATGAGAC 469
```

Db	364	CTGGCCAGCCAGTGTGAGAGAAAAAGACCGAATGTGCCTTTAAGAAGAAGAGCAATGAGAC	423
Qy	470	ACAGTGTTTCAACTTCATCCGTGTCTGGTTTCTTACAATGTCACCCATCTCTACACCTG	529
Db	424	ACAGTGTTTCAACTTCATTCGAGTCTGGTCTCTTACAATGCTACTCACCTCTATGCCTG	483
Qy	530	CGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATT-----	566
Db	484	TGGGACCTTTGCCTTCAGCCCTGCCTGTACCTTCATTACGTGCGACCCTGGCATTCCTGGG	543
Qy	567	-----GAACTTCAAGATTCCCTACCTGTTGCCCATCTCGGAG	602
Db	544	CTCCCAGCCTCTTCCCCCTCTAGGAACTCCAAGATTCCCTCCTGTTGCCCATCTTGATA	603
Qy	603	GACAAGGTCATGGAGGGAAAAGGCCAAAGCCCTTTGACCCCGCTCACAAGCATACGGCT	662
Db	604	GACAAGGTCATGGACGGGAAGGGCCAAAGCCCTTTGACCTGTTTACAAGCACACAGCT	663
Qy	663	GTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTTCTGGGCAGTGAGCCC	722
Db	664	GTCTTGGTGCATGGGATGCTTTATTCCGGCACCATGAACAACCTTCTGGGCAGCGAGCCC	723
Qy	723	ATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTTCTCCGCTGG	782
Db	724	ATCCTGATGCGGACACTGGGATCCCAGCCTGTTCTCAAGACTGACATCTTCTTACGCTGG	783
Qy	783	CTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTC	842
Db	784	CTGCACGCGGATGCCTCCTTCGTGGCAGCCATTCATCCACCCAGGTCGTCTATTTCTTC	843
Qy	843	TTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGTGGCT	902
Db	844	TTTGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAAGAGCTGTATATATCCAGGTGGCT	903
Qy	903	AGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTC	962
Db	904	CAAGTCTGCAAGAACGACGTGGGCGGTGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTC	963
Qy	963	CTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTTCATCCGCCAC	1022
Db	964	CTCAAAGCCCAGTTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCCGCCAC	1023
Qy	1023	GCGGTCTGTCTCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCC	1082
Db	1024	GCGGTCTGTCTGCCCGCCGATTCTCCCTCTGTTTCCCGCATCTACGCAGTCTTTACCTCC	1083
Qy	1083	CAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATT	1142
Db	1084	CAGTGGCAGGTTGGCGGGACCAGGAGCTCAGCAGTCTGTGCCTTCTCTCTCACGGACATT	1143
Qy	1143	GAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACT	1202
Db	1144	GAGCGAGTCTTTAAAGGGGAAGTACAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACT	1203
Qy	1203	TATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGAT	1262

Db 1204 TACCGGGGCTCAGAGGTCAGCCCCAGGCCAGGCAGTTGCTCCATGGGCCCCCTCCTCTGAC 1263

Qy 1263 AAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCC 1322
 || ||| |||||||||||||||||||| |||||||||||| |||| || || |||

Db 1264 AAAGCCTTGACCTTCATGAAGGACCATTTTCTGATGGATGAGCACGTGGTAGGAACACCC 1323

Qy 1323 CTGCTGGTCAAATCTGGCGTGGAGTATACACGGCTTGCACTGGAGACAGCCCAGGGCCTT 1382
 |||||||| |||| |||||||| |||||||||| |||||| |||| | |||||||

Db 1324 CTGCTGGTGAAGTCTGGTGTGGAGTACACACGGCTTGCTGTGGAGTCAGCTCGGGGCCTT 1383

Qy 1383 GATGGGCACAGCCATCTTGTCTGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCT 1442
 ||||| |||||| | |||||| |||| || |||| |||| | |||||||

Db 1384 GATGGGAGCAGCCATGTGGTCTGTATCTGGGTACCTCCACGGGGTCCCTGCACAAGGCT 1443

Qy 1443 GTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGGAAGAGATTGAGCTGTTCCCTGACCCT 1502
 |||| | |||||||||| || || |||| |||||||||| |||||| ||

Db 1444 GTGGTGCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATTGAGCTGAGCCCTGACTCT 1503

Qy 1503 GAACCTGTTTCGCAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTCA 1562
 || |||||| |||||||||||||||||| |||||||||||||| |||||||

Db 1504 GAGCCTGTTTCGAAACCTGCAGCTGGCCCCCGCCAGGGTGCAGTGTTTGCAGGCTTCTCT 1563

Qy 1563 GGAGGTGTCTGGAGGGTGGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGT 1622
 |||| |||||| || ||| | |||| || |||||| ||||||||||||||

Db 1564 GGAGGCATCTGGAGAGTCCCAGGGCCAATTGCAGTGTCTACGAGAGCTGTGTGGACTGT 1623

Qy 1623 GTCCTTGCCCGGGACCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTG 1682
 || || | |||||| |||||||||||||| || || || || || |||

Db 1624 GTGCTGCNCAGGGACCCTCACTGTGCCTGGGACCCTGAATCAAGACTCTGCAGCCTTCTG 1683

Qy 1683 TCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGAACCCAGAGTGGGCA 1742
 |||| || || || || || |||||||||| || || || || || |||

Db 1684 TCTGGCTCTACC---AAGCCTTGGAAGCAGGACATGGAACGCGGCAACCCGGAGTGGGTA 1740

Qy 1743 TGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1802
 || || |||||| || |||||| || || |||||| || || || || || |||

Db 1741 TGCACCCGTGGCCCCATGGCCAGGAGCCCCCGGCGTCAGAGCCCCCTCAACTAATTAA 1800

Qy 1803 GAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTG 1862
 |||||| || |||||||||||||||||| |||||||||||||| || ||

Db 1801 GAAGTCCTGACAGTCCCCAACTCCATCCTGGAGCTGCCCTGCCCCACCTGTCAGCACTG 1860

Qy 1863 GCCTCTTATTATTGGAGTCATGGCCAGCAGCAGTCCAGAAAGCCTCTTCCACTGTCTAC 1922
 |||||| || |||||| || || || |||||| || || || || || |||

Db 1861 GCCTCTTACCCTGGAGTCATGGCCGAGCCAAAATCTCAGAAAGCCTCTGCTACCGTCTAC 1920

Qy 1923 AATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGTCTCTACAGTGCTGGGCA 1982
 |||||||||| || || |||||| || || || |||||| || ||

Db 1921 AATGGCTCCCTCTTGCTGCTGCCGCAGGATGGTGTGCGGGGCCTCTACAGTGTGTGGCG 1980

Qy 1983 ACTGAGAATGGCTTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACC 2042
 |||||| || || |||||| || |||||| || || || |||||| || ||

Db 1981 ACTGAGAACGGCTACTCATACCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCAGCCC 2040

Qy 2043 CTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACC 2102
 |||| |||| |||| |||| || | |||| |||| || |||||| ||||

Db 2041 CTGGCGCTGGACCCTGAGCTGGCGGGCGTTCCCCGTGAGCGTGTGCAGGTCCCGCTGACC 2100

Qy	2103	AGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGAGTCCCTACTGGCCCCACTTTGTCACT	2162
Db	2101	AGGGTCGGAGGCGGAGCTTCCATGGCTGCCAGCGTCTACTGGCCCCATTTTCTCATC	2160
Qy	2163	GTCAGTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCA	2222
Db	2161	GTTACCGTCTCTCGGCCATCGTGCTCCTGGGAGTGCTCACTCTCCTCCTCGCTTCCCCA	2220
Qy	2223	TTGAGAGCACCTCCGGGCTCGGGGGCAAGGTTTCAGGGCTGTGAGACCCGTGCGCCCTGGGGAG	2282
Db	2221	CTGGGGGGCGCTGCGGGCTCGGGGTAAGGTTTCAGGGCTGTGGGATGCTGCCCCCAGGGAA	2280
Qy	2283	AAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCC	2342
Db	2281	AAGGCTCCACTGAGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCC	2340
Qy	2343	AGTGATGTGGACGCTGACAACAAC'TGCC'TAGGCAGT'GAGGTAGCT'TAAAC'TCTAGGCACA	2402
Db	2341	AGTGACGTAGATGCCGACAACAACCATCTGGGCGCCGAAGTGGCT'TAAACAGGGACACAG	2400
Qy	2403	GGCCGGGGCT--GCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC	2460
Db	2401	ATCCGCAGCTGAGCAGAGCAAGCCACTGGCCTTGTTGGCTATGC-----	2444
Qy	2461	TGACTAGGATGACAGCAGCACAAAAGACCACCTTCTCCCTGAGAGGAGCTTCTGCTAC	2520
Db	2445	-----CAGGCACAGTGCCACTCTGACCAGGGTAGGAGGCTCTCCTGCTAA	2489
Qy	2521	TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC	2580
Db	2490	CGTGTGTACCTACAGACCCAGTAGGT-----CCTCCCCTGTGGGAC	2532
Qy	2581	TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC	2640
Db	2533	TCTCTTCTGCAAGCACATTGGGCTGTCT-----CCATACCTGTACT	2573
Qy	2641	TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC	2700
Db	2574	TGTGCTGTGACAGGAAGAGCCAGACAGGTTTCTTTGATTTTGATTGACCCAAGAGCCCTC	2633
Qy	2701	CAGAAACACAGTGT'TTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA	2760
Db	2634	CTGTAACAAACGTGCTCCAGGAGACCATGAAAGGTGTGGCTGTCTGGGATTCTGTGGTGA	2693
Qy	2761	TGAACACCAAACATCTAAACAATCATATGCTA-----ACATGCCACTCCTGGAAACTC	2813
Db	2694	CAAAC-CTAAGCATCCGAGCAAGCTGGGGCTATTTCCTGCAAACCTCCATCCTGAACGCTGT	2752
Qy	2814	CACTCT----GAAGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAG	2868
Db	2753	CACTCTAGAAGCAGCTGCTGCTTTGAACACCAGCCCACCTCCTTCCCAAGAGTCTCTAT	2812
Qy	2869	GGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTT	2928
Db	2813	GGAGTTGGCCCCCTTGTTTTCCTTTACCAGTCATGCCATACTGTTT---GGGAAGTCATC	2869

Qy	2929	CCTGAAGTCTGACCACCTTTCTTCCTTGCTTCAGTTGGGGCAGACTCTGATCCCT---	TCT	2985
Db	2870	TCTGAAGTCTAACCACCTTCCTTCCTTGCTTCAGTTTGGACAGATTGTTATTATTGTCTCT		2929
Qy	2986	GCCCTGGC-AGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACC		3044
Db	2930	GCCCTGGCTAGAATGGGGGGCATAATCTGAGCCTTGTTCCCTTGTCAGTGTGGCTGACC		2989
Qy	3045	CCTTCACCTCTCCCCCTCCCCTTTTCTTTGTTTTGGGATT CAGAAA ACTGCTTGT CAGAG		3104
Db	2990	CTTGACCTCTT--CCTTCCTCCTCCCCTTTGTTTTGGGGATT CAGAAA ACTGCTTGT CACAG		3047
Qy	3105	ACTGTTTATTTTTTTATTAAAAA		3126
Db	3048	ACAATTTATTTTTTTATTAAAAA		3069

Query Match 43.7%; Score 1372.2; DB 9; Length 2172;
Best Local Similarity 71.9%; Pred. No. 0;
Matches 1560; Conservative 0; Mismatches 611; Indels 0; Gaps 0;

```
Qy      105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164
          ||||| ||| ||||| |||| | |||| |||| | ||| |||||
Db      1  ATGGCCCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTTTTTCTTCCAA 60

Qy      165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 224
          || | | |||| | | | | | | | | | | |||||
Db      61 CTCTTCCTGCTGCCATCACTGCCACCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCCC 120

Qy      225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
          || |||| |||| |||| | | | | | |||| | ||||| ||| |||
Db      121 AGAGTCAAATACCATGCTGGAGACGGGCACAGGGCCCTCAGCTTCTTCCAACAAAAGGC 180

Qy      285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACCTCTACGTGGGGGCT 344
          |||| | ||||| ||||| ||||| |||| | ||||| |||||
Db      181 CTCCGAGACTTTGACACGCTGCTCCTGAGTGACGATGGCAACACTCTCTATGTGGGGGCT 240

Qy      345 CGAGAAGCCATTCTGGCCTTGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATG 404
          |||| | ||| | ||||| ||||| | |||| | ||| |||||
Db      241 CGAGAGGCCGTCCTGGCCTTGAATATCCAGAACCAGGAATCCAAGGCTAAAGAACATG 300

Qy      405 ATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
          |||| | ||||| ||||| ||||| ||||| ||||| |||||
Db      301 ATACCCTGGCCAGCCAGTGAGAGAAAAAGACCGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy      465 GAGACACAGTGTTCACCTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
          ||||| ||||| ||||| ||| ||||| ||||| || || ||||
Db      361 GAGACACAGTGTTCACCTTCATTCGAGTCCGGTCTCTTACAATGCTACTCACCTCTAT 420

Qy      525 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGACCTTCATTGAACCTCAAGATTCCCTAC 584
          |||| | |||| | ||||| ||||| ||||| ||||| |||
Db      421 GCCTGTGGGACCTTTGCCTTCAGCCCTGCCTGTACCTTCATTGAACCTCAAGATTCCCTC 480

Qy      585 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCCCTTTGACCCC 644
          ||||| ||||| | ||||| ||||| || | ||||| |||||
Db      481 CTGTTGCCCATCTTGATAGACAAGGTCATGGACGGGAAGGGCAAAGCCCCCTTTGACCT 540

Qy      645 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
          | ||||| || | ||||| ||||| ||||| || | |||||
Db      541 GTTCACAAGCACACAGCTGTCTTGGTCGATGGGATGCTTTATTCCGGCACCATGAACAAC 600

Qy      705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCAAGACC 764
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      601 TTCCTGGGCAGCGAGCCCATCCTGATGCGGACACTGGGATCCCAGCCTGTTCTCAAGACT 660

Qy      765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
          |||| ||| | |||||
Db      661 GACATCTTCTTACGCTGGCTGCACGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720

Qy      825 CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC 884
Db      721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780

Qy      885 CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG 944
```

[illegible]

Db 1621 GGCAACCCGGAGTGGGTATGCACCCGTGGCCCCATGGCCAGGAGCCCCCGGCGTCAGAGC 1680

Qy 1785 CGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC 1844
| ||| ||| | ||||| ||||| | ||||| ||||| ||||| |||||

Db 1681 CCCCCTCAACTAATTAAAGAAGTCCTGACAGTCCCCAACTCCATCCTGGAGCTGCCCTGC 1740

Qy 1845 CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCAGCAGCAGTCCCAGAA 1904
||||| ||||| ||||| | ||||| ||||| ||| | |||||

Db 1741 CCCCACCTGTCAGCACTGGCCTCTTACCACTGGAGTCATGGCCGAGCCAAAATCTCAGAA 1800

Qy 1905 GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT 1964
||||| | || ||||| ||||| ||||| | ||||| || |||||

Db 1801 GCCTCTGCTACCGTCTACAATGGCTCCCTCTTGCTGCTGCCGCAGGATGGTGTCTGGGGGC 1860

Qy 1965 CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG 2024
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1861 CTCTACCAGTGCTGTGGCGACTGAGAACGGCTACTCATACCCTGTGGTCTCCTATTGGGTA 1920

Qy 2025 GACAGCCAGGACCAGACCCCTGGCCCTGGATCCTGAAC TGGCAGGCATCCCCGGGAGCAT 2084
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1921 GACAGCCAGGACCAGCCCCCTGGCGCTGGACCCTGAGCTGGCGGGCGTTCCCCGTGAGCGT 1980

Qy 2085 GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTAC 2144
||| ||||| ||||| ||||| | || || || || ||||| |||||

Db 1981 GTGCAGGTCCCGCTGACCAGGGTCGGAGGCGGAGCTTCCATGGCTGCCCAGCGGTCTTAC 2040

Qy 2145 TGGCCCCACTTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC 2204
||||| ||| ||| || || ||||| ||| || ||||| ||||| |||||

Db 2041 TGGCCCCATTTTCTCATCGTTACCGTCTCTCTGGCCATCGTGCTCCTGGGAGTGCTCACT 2100

Qy 2205 ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG 2264
|||| | || ||||| || | || || ||||| ||||| ||||| |||||

Db 2101 CTCTCTCTCGCTTCCCCACTGGGGGCGCTGCGGGCTCGGGGTAAGGTTTCAGGGCTGTGGG 2160

Qy 2265 ACCCTGCGCCC 2275
| |||| |||

Db 2161 ATGCTGCCCCC 2171

RESULT 8

BX367242/c

LOCUS BX367242 1108 bp mRNA linear EST 27-APR-2004

DEFINITION BX367242 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL002Y004 3-PRIME, mRNA sequence.

ACCESSION BX367242

VERSION BX367242.2 GI:46625363

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1108)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 8, 2003 this sequence version replaced gi:30455608.
Contact: Genoscope

Db	691	CATGCTGGCTGGGCGGCCCAAGMACAGCCCTGACTAGGATSACAGCAGCACAAAAGACCA	632
Qy	2491	CCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG	2550
		: :	
Db	631	CCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATMACTGATVACACTCAGCAGGGTG	572
Qy	2551	ATGCACAGCAGTCTGCCTCCCTTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAA	2610
Db	571	ATGAACAGCAGTCTGCCTCCCTTATGGAACCTCCCTTCTACCAAGCACATGAGCTCTCTAA	512
Qy	2611	CAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGAT	2670
Db	511	CAGGGTGGGGGCTACCCCCAGACCTGCTCCTAAACTGATATTGAAGAACCTGGAGAGGAT	452
Qy	2671	CCTTCAGTTCTGGCCATTCCAGGGACCTCCAGAAACACAGTGTTTCAAGAGACCCTAAA	2730
Db	451	CCTTCAGTTCTGGCCATTCCAGGGACCTCCAGAAACACAGTGTTTCAAGAGACCCTAAA	392
Qy	2731	AAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGC	2790
		:	
Db	391	AAACCTGCMTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAAAAATAATATGC	332
Qy	2791	TAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCT	2850
		: : : :	
Db	331	TAAMATGCAACTCCTGGAAACTCMAMTCTGAAGCTGCCGCTTTGAAMACCAAACACTCCCT	272
Qy	2851	TCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCT	2910
		:	
Db	271	TCTCCCAGGGTCATGMAGGGATCTGCTCCCTCCTGCTTCCCTTACMAGTCGTGMACAGCT	212
Qy	2911	GACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCCTTCTTGCTTCAGTTGGGGCAG	2970
Db	211	AACTCCCAGGAAGTCTTCCCTGAAGTCTGACCACCTTTCNTCTAGCTTAAGTTGGRGAAA	152
Qy	2971	ACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGTAATCTGAGCCTTCTTCACTCCTT	3030
Db	151	ACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGTAATNTGAGCCTTCTTAACTCCTT	92
Qy	3031	TACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTAGAAA	3090
Db	91	TACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTAGAAA	32
Qy	3091	ACTGCTTGTGAGAGACTGTTTATTTTTTTATT	3121
Db	31	ACTGCTTGTGAGAGACTGTTTCBYTTTTCTT	1

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1064)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 5, 2003 this sequence version replaced gi:30384744.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 907.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CS0DL005AB09NP1&c=907.f>.

FEATURES

source Location/Qualifiers

1. .1064

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DL005YC17"

/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"

/cell_line="RAMOS CELL LINE"

/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 29.5%; Score 926.2; DB 5; Length 1064;
Best Local Similarity 95.5%; Pred. No. 1.2e-233;
Matches 1000; Conservative 15; Mismatches 24; Indels 8; Gaps 6;

Qy 2058 GAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGG 2117
|| ||| |||| | || | : |:||||||||||| :|||||||||||

Db 1040 GATCTGAATGGCAGCATCCCCGGGAGMWGKGARGTCCCGTTGACC-RGGTCAGTGGTGGG 982

Qy 2118 GCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTT 2177
| || | :|||||||||||:|:|| ||| |||||||||||||||||||

Db 981 --CCGCCCTGGYGCCAGCAGTCCWAYTG--CCCCATTTGTCACTGTCACTGTCTCTTT 926

Qy 2178 GCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGG 2237
||||||||||||| ||||||||||||||| |||||||||||||||

Db 925 GCCTTAGTGCTTTCA-GAGCCCTCATCATCCTCGT-GCCTCCCCATTGAGAGCACTCCGG 868

Qy 2238 GCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTTAAGC 2297
||||||||||||| ||||||||||||||| |||||||||||||||

Db 867 GCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTTAAGC 808

Qy 2298 AGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCT 2357
||||||||||||| ||||||||||||||| |||||||||||||||

Db	807	AGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCT	748
Qy	2358	GACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT	2417
Db	747	GACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT	688
Qy	2418	GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA	2477
Db	687	GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA	628
Qy	2478	GCACAAAAGACCACCTTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC	2537
Db	627	GCACAAAAGACCACCTTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC	568
Qy	2538	ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC	2597
Db	567	ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC	508
Qy	2598	ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA	2657
Db	507	ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA	448
Qy	2658	ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC	2717
Db	447	ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC	388
Qy	2718	AAGAGACCCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTA	2777
Db	387	AAGAGACCCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTA	328
Qy	2778	AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC	2837
Db	327	AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC	268
Qy	2838	ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA	2897
Db	267	ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA	208
Qy	2898	GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCCTGAAGTCTGACCACCTTCTTCTTGCT	2957
		:	
Db	207	GTCGTGCACCGCTGACTYCCAGGAAGTCTTCCCTGAAKTCTGACCACCTTCTTCTTGCT	148
Qy	2958	TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG-CAGGGGTAATCTGAGC	3016
		: : :	
Db	147	TCAGTTGGGGCAGAYTYTGATCCCTTCTGCCCTGGYAGAATGGTCAGGGGTAATCTGAGC	88
Qy	3017	CTTCTTCACTCCTTTACCCTAGCTGACCCCTTACCTCTCCCCCTCCCTTTTCTTGT	3076
		: : :	
Db	87	CTTCTTCACTCCTTTACCCTAGCTGACCCCTTMCCTCTCCCBTSSCTTTTCTTGT	28
Qy	3077	TTGGGATTTCAGAAAACCTGCTTGTGTCAGA	3103
Db	27	TTGGGATTTCAGAAAACCTGCTTGTGTCAGA	1

LOCUS BX350606 922 bp mRNA linear EST 08-APR-2004
 DEFINITION BX350606 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
 Homo sapiens cDNA clone CS0DL005YC17 3-PRIME, mRNA sequence.
 ACCESSION BX350606
 VERSION BX350606.1 GI:30373499
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 922)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 907.f
 For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAI043ZD06_CS04076_1&c=907.f.
 FEATURES Location/Qualifiers
 source 1. .922
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DL005YC17"
 /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
 /cell_line="RAMOS CELL LINE"
 /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN

Query Match 27.8%; Score 874.4; DB 5; Length 922;
 Best Local Similarity 98.7%; Pred. No. 6.1e-220;
 Matches 878; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1372 CCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGC 1431
 ||||| |||||||||||||||||||||||||||| ||||||| |||||||||
 Db 919 CCCAGGNCCTTGATGGGCACAGCCATCTTGTCATGTACTTGGGAACCACAACAGGGTCGC 860
 Qy 1432 TCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGGAAGAGATTTCAGCTGT 1491
 ||||| |||||||||||||||||||||||||||| ||||||| |||||||||
 Db 859 TCCACAAGACTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGGAAGAGATTTCAGCTGT 800
 Qy 1492 TCCCTGACCCTGAACCTGTTTCGAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTG 1551
 ||||||||| |||||||||||||||||||||||| ||||| |||||||||
 Db 799 TCCCTGACCCTGANCTGTTTCGAACCTGCAGCTGGCCNCCACCAAGGGTGCAGTGTTGN 740

Qy	1552	TAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTATGAGAGCT	1611
Db	739	TAGGCTTCTCAGNAGGTGTCTGGAGGGTGCNCCGAGCCAACCTGTAGTGTCTATGAGAGCT	680
Qy	1612	GTGTGGACTGTGTCCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCT	1671
Db	679	GTGTGGACTGTGTCCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCT	620
Qy	1672	GTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACC	1731
Db	619	GTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACC	560
Qy	1732	CAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGC	1791
Db	559	CAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGC	500
Qy	1792	AAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACC	1851
Db	499	AAATCATTAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGAGCTCCCCTGCCCCCACC	440
Qy	1852	TGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTT	1911
Db	439	TGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTT	380
Qy	1912	CCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACC	1971
Db	379	CCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACC	320
Qy	1972	AGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCC	2031
Db	319	AGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCC	260
Qy	2032	AGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGG	2091
Db	259	AGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGG	200
Qy	2092	TCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCC	2151
Db	199	TCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCC	140
Qy	2152	ACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCG	2211
Db	139	ACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCG	80
Qy	2212	TGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGT	2261
Db	79	TGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGT	30

RESULT 11

BX384966

LOCUS BX384966 934 bp mRNA linear EST 23-APR-2004

DEFINITION BX384966 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL005YC17 5-PRIME, mRNA sequence.

ACCESSION BX384966

VERSION BX384966.2 GI:46556002

KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 934)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 8, 2003 this sequence version replaced gi:30436505.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 907.f
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CS0DL005AB09QP1&c=907.f>.
 FEATURES Location/Qualifiers
 source 1. .934
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DL005YC17"
 /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
 /cell_line="RAMOS CELL LINE"
 /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN
 Query Match 27.0%; Score 849.2; DB 5; Length 934;
 Best Local Similarity 97.0%; Pred. No. 2.9e-213;
 Matches 871; Conservative 4; Mismatches 22; Indels 1; Gaps 1;
 Qy 99 CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC 158
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC 60
 Qy 159 TTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCC 218
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 TTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCC 120
 Qy 219 ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG 278
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG 180
 Qy 279 AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG 338
 |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
 Db 181 AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG 240

Qy	339	GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAG	398
Db	241	GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAG	300
Qy	399	AACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAG	458
Db	301	AACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAG	360
Qy	459	AGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAATGTCACCCAT	518
Db	361	AGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAATGTCACCCAT	420
Qy	519	CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGAT	578
Db	421	CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGAT	480
Qy	579	TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT	638
Db	481	TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT	540
Qy	639	GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG	698
Db	541	GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG	600
Qy	699	AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC	758
Db	601	AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC	660
Qy	759	AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT	818
Db	661	AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT	720
Qy	819	TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG	878
Db	721	TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG	780
Qy	879	AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG	938
Db	781	AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCG-AAARCTG	839
Qy	939	CTGCAGAAGAAGTGGACCACCTTCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGC	996
Db	840	CTGCAGAAGAAGTGGACCMCTCCTGAAGCCCACYGCYCTCMCCAGCCCGGGCACTGC	897

RESULT 12

BX328255

LOCUS BX328255 897 bp mRNA linear EST 07-APR-2004

DEFINITION BX328255 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL005YC17 5-PRIME, mRNA sequence.

ACCESSION BX328255

VERSION BX328255.2 GI:46262160

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 897)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 1, 2003 this sequence version replaced gi:30307730.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
907.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAG053ZH06_CS05040_1&c=907.f.

FEATURES
source Location/Qualifiers
1. .897
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL005YC17"
/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 26.7%; Score 839; DB 5; Length 897;
Best Local Similarity 99.0%; Pred. No. 1.5e-210;
Matches 886; Conservative 0; Mismatches 5; Indels 4; Gaps 4;

Qy 805 TGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGG-AGACAGCCAGCGAG 863
|||||
Db 1 TGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAAGACAGCCAGCGAG 60

Qy 864 TTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTG 923
|||||
Db 61 TTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTG 120

Qy 924 GGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGC 983
|||||
Db 121 GGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGC 180

Qy 984 ACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGAT 1043
|||||
Db 181 ACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGAT 240

Qy 1044 TCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCAGTGGCAGGTTGGCGGGACC 1103
|||||
Db 241 TCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCAGTGGCAGGTTGGCGGGACC 300

Qy 1104 AGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAA 1163
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 AGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAA 360

Qy 1164 TACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGGCCCTGAGACCAAC 1223
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 TACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGGCCCTGAGACCAAC 420

Qy 1224 CCCC GCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAG 1283
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 CCCC GCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAG 480

Qy 1284 GACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTG 1343
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 GACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTG 540

Qy 1344 GAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTC 1403
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 GAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTC 600

Qy 1404 ATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT 1463
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 ATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT 660

Qy 1464 GCTCATCTGGTGGAAGAGATTTCAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAG 1523
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 GCTCATCTGGTGGAAGAGATTTCAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAG 720

Qy 1524 CTGGCCCCCACCAGGGTGCA-GTGT TGTAGGCTTCTCAGGAGGTGTCTGG-AGGGTGC 1581
 |||||||||||| ||||| |||||||||||||||||||||||||||| |||||
 Db 721 CTGGCCCCCACCAGGTGCANGTGT TGTAGGCTTCTCAGGAGGTGTCTGGNAGGGTGC 780

Qy 1582 CCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCCGGGACCCCC 1641
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 781 CCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCCGGGACCCCC 840

Qy 1642 ACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCT 1696
 |||||||||||||||||||||||| |||||||| ||||||||||||||||
 Db 841 -CTGTGCCTGGGACCCTGAGTCCCGACCCTGTTGCCTTCTGTCTGCCCCCAACCT 894

RESULT 13

BQ057192

LOCUS BQ057192 974 bp mRNA linear EST 29-MAR-2002

DEFINITION AGENCOURT_6769628 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5812383
 5', mRNA sequence.

ACCESSION BQ057192

VERSION BQ057192.1 GI:19816532

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 974)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2062 row: 1 column: 16
High quality sequence stop: 714.

FEATURES Location/Qualifiers
source 1. .974
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5812383"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 26.3%; Score 827.4; DB 5; Length 974;
Best Local Similarity 92.6%; Pred. No. 1.8e-207;
Matches 902; Conservative 0; Mismatches 67; Indels 5; Gaps 3;

```

Qy      92 TCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCT 151
      |||
Db      1 TCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCT 60

Qy     152 TTTCTCTTCCAAGTCTTCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCA 211
      |||
Db      61 TTTCTCTTCCAAGTCTTCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCA 120

Qy     212 GGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTT 271
      |||
Db     121 GGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTT 180

Qy     272 CCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCT 331
      |||
Db     181 CCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCT 240

Qy     332 CTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAG 391
      |||
Db     241 CTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAG 300

Qy     392 GCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAA 451

```

Db	301		GCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAA	360
Qy	452		GAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGT	511
Db	361		GAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGT	420
Qy	512		CACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACT	571
Db	421		CACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACT	480
Qy	572		TCAAGATTCTTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAG	631
Db	481		TCAAGATTCTTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAG	540
Qy	632		CCCCTTTGACCCCGCTCACAAGCATACGGCTGTCCTTGGTGGATGGGATGCTCTATTCTGG	691
Db	541		CCCCTTTGACCCCGCTCACAAGCATACGGCTGTCCTTGGTGGATGGGATGCTCTATTCTGG	600
Qy	692		TACTATGAACAACCTTCTTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCC	751
Db	601		TACTATGAACAACCTTCTTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCC	660
Qy	752		TGTCCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGC	811
Db	661		TGTCCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGC	720
Qy	812		CATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTT	871
Db	721		CATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTT	780
Qy	872		CTTTGAGAGGCTCCACACATCGCGGGTGG-CTAGAGTCTGCAAGAATGACGTGGGC-GGC	929
Db	781		CTTTGAGAGGCCCCACCCTCCCGGGGGCCCTANAGTCTGCCAAAATGACGTGGGCGGGC	840
Qy	930		GAAAAGCTGCTGCAGAAGAA---GTGGACCACCTTCTTGAAGGCCAGCTGCTCTGCACC	986
Db	841		GAAAAGCTGCTGCAAAAAAAGTGGACCCCCCTTCTTGAAGGCCAGCTGCTCTGGCCC	900
Qy	987		CAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCT	1046
Db	901		CCAGCCGGGGGAGCTTGCCCTTTCACGTCATTCCCGCCCCCGGGTCTGGCTCCCCC	960
Qy	1047		CCCACAGCTCCCCA	1060
Db	961		CCGAATTTTCCCCA	974

RESULT 14

BX390196

LOCUS BX390196 944 bp mRNA linear EST 29-APR-2004

DEFINITION BX390196 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens cDNA clone CS0DD003YE08 5-PRIME, mRNA sequence.

ACCESSION BX390196

VERSION BX390196.2 GI:46873199

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 944)

AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 8, 2003 this sequence version replaced gi:30463276.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
907.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAG009ZD12_CS00860_1&c=907.f.

FEATURES Location/Qualifiers

source 1. .944
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD003YE08"
/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 26.1%; Score 820.4; DB 5; Length 944;
Best Local Similarity 97.4%; Pred. No. 1.3e-205;
Matches 897; Conservative 0; Mismatches 17; Indels 7; Gaps 6;

Qy 1535 CCAGGGTGCAGTGTGTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTG 1594
|||||

Db 1 CCAGGGTGCAGTGTGTTGTAGGCTTCT-AGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTG 59

Qy 1595 TAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGA 1654
|||||

Db 60 TAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGA 119

Qy 1655 CCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGA 1714
|||||

Db 120 CCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGA 179

Qy 1715 CATGGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCG 1774
|||||

Db 180 CATGGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCG 239

Qy 1775 GCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGA 1834
|||||

Db 240 GCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGA 299

Qy	1835	GCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGC	1894
Db	300	GCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGC	359
Qy	1895	AGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGG	1954
Db	360	AGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGG	419
Qy	1955	AGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTC	2014
Db	420	AGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTC	479
Qy	2015	CTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCC	2074
Db	480	CTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCC	539
Qy	2075	CCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCCA	2134
Db	540	CCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCCA	599
Qy	2135	GCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTTCAGG	2194
Db	600	GCAGTCCTACTGGCCCCACTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTTCAGG	659
Qy	2195	AGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTC-	2253
Db	660	AGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTTCGGGCAAGGTTCA	719
Qy	2254	AGGGCTGTGAGACCCTGCGCCCTGGGG--AGAAGGCCCGTTAAGCAGAGAGCAACA-CC	2310
Db	720	AGGGCTGTGAGACCCTGCGCCCTGGGGGAGAAGGGCCCGTTAAGCAGAGAGCAACACCC	779
Qy	2311	TCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACG-CTGACAACAACCTGC	2369
Db	780	TTCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGGCGCCTGACAACAACCTGC	839
Qy	2370	CTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGG	2429
Db	840	CTAGGCACTGAGGTAGCTTAAACTCTA-GCACAGCCCGGGCTTGCGGGGCAGCCACCTGC	898
Qy	2430	CCATGCTGGCTGGGCGGCCCA	2450
Db	899	CCATGCTGTGTGGGCGGCCCA	919

RESULT 15

CB243787/c

LOCUS CB243787 797 bp mRNA linear EST 12-FEB-2003

DEFINITION UI-CF-FN0-agg-a-05-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
UI-CF-FN0-agg-a-05-0-UI 3', mRNA sequence.

ACCESSION CB243787

VERSION CB243787.1 GI:28365431

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 797)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA sequence: 1-46, >AT_rich#Low_complexity (matched compliment)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES Location/Qualifiers

source 1. .797
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FN0-agg-a-05-0-UI"
 /tissue_type="Human Lung Epithelial cells"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-FN0"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-FN0 is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu
 TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h
 TAG_LIB=UI-CF-FN0
 TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 24.8%; Score 779.8; DB 6; Length 797;
 Best Local Similarity 99.4%; Pred. No. 7e-195;
 Matches 781; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2358 GACAACAAGTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT 2417
 ||||||||||| ||||||||||||||||||| |||||||||||||||||||
 Db 797 GACAACAAGTGCNTAGGCACTGAGGTAGCTTAAACTNTAGGCACAGGCCGGGGCTGCGGT 738

Qy	2418	GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA	2477
Db	737	GCAGGCACCCGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGANTAGGATGACAGCA	678
Qy	2478	GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC	2537
Db	677	GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC	618
Qy	2538	ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC	2597
Db	617	ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC	558
Qy	2598	ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA	2657
Db	557	ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA	498
Qy	2658	ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCCTCCAGAAACACAGTGTTTC	2717
Db	497	ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCCTCCAGAAACACAGTGTTTC	438
Qy	2718	AAGAGACCCATAAAAAACCTGCCTGTCCCAGGACCCCTATGGTAATGAACACCAAACATCTA	2777
Db	437	AAGAGACCCATAAAAAACCTGCCTGTCCTAGGACCCCTATGGTAATGAACACCAAACATCTA	378
Qy	2778	AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC	2837
Db	377	AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC	318
Qy	2838	ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA	2897
Db	317	ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA	258
Qy	2898	GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCT	2957
Db	257	GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCT	198
Qy	2958	TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCC	3017
Db	197	TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCC	138
Qy	3018	TTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTT	3077
Db	137	TTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTT	78
Qy	3078	TGGGATTCAGAAAAGTCTTGTCTGAGAGCTGTTTATTTTTTATTAAAAATATAAGGCTTA	3137
Db	77	TGGGATTCAGAAAAGTCTTGTCTGAGAGCTGTTTATTTTTTATTAAAAATATAAGGCTTA	18
Qy	3138	AAAAAA 3143	
Db	17	AAAAAA 12	

Search completed: February 15, 2005, 13:17:35
Job time : 9877 secs

OM nucleic - nucleic search, using sw model

Run on: February 14, 2005, 19:11:26 ; Search time 1686 Seconds
(without alignments)
10999.493 Million cell updates/sec

Title: US-10-015-391A-276
Perfect score: 3143
Sequence: 1 gggctgaggcactgagagac.....aaatataaggcttaaaaaaa 3143

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
37	3143	100.0	3143	16	US-10-013-909A-276	Sequence 276, App	
66	3060.8	97.4	3505	16	US-10-051-835-13	Sequence 13, Appl	
67	3040.8	96.7	3104	10	US-09-759-130B-387	Sequence 387, App	
68	3040.8	96.7	3104	13	US-10-042-431-17	Sequence 17, Appl	
69	3040.8	96.7	3104	18	US-10-741-790-387	Sequence 387, App	
70	3035.8	96.6	3191	15	US-10-050-882-11	Sequence 11, Appl	
71	3029.8	96.4	3042	9	US-09-774-434-5	Sequence 5, Appli	
72	2860.4	91.0	3146	18	US-10-489-372-49	Sequence 49, Appl	
73	2682.2	85.3	2981	17	US-10-104-047-319	Sequence 319, App	
74	2476.4	78.8	2768	17	US-10-470-360-35	Sequence 35, Appl	
75	2437	77.5	2745	18	US-10-489-372-32	Sequence 32, Appl	
76	2283	72.6	2283	10	US-09-759-130B-388	Sequence 388, App	
77	2283	72.6	2283	13	US-10-042-431-18	Sequence 18, Appl	
78	2283	72.6	2283	18	US-10-741-790-388	Sequence 388, App	
c 79	2281	72.6	2281	17	US-10-190-115-9	Sequence 9, Appli	
c 80	2281	72.6	2281	17	US-10-369-072-9	Sequence 9, Appli	
81	2228.4	70.9	2271	17	US-10-190-115-7	Sequence 7, Appli	
82	2228.4	70.9	2271	17	US-10-369-072-7	Sequence 7, Appli	
83	2104.8	67.0	2238	18	US-10-489-372-50	Sequence 50, Appl	
84	1727.6	55.0	3046	10	US-09-759-130B-447	Sequence 447, App	
85	1727.6	55.0	3046	13	US-10-042-431-71	Sequence 71, Appl	
86	1727.6	55.0	3046	13	US-10-042-431-77	Sequence 77, Appl	
87	1727.6	55.0	3046	18	US-10-741-790-447	Sequence 447, App	
88	1015.8	32.3	1674	9	US-09-728-952-38	Sequence 38, Appl	
c 89	576	18.3	576	16	US-10-029-386-25944	Sequence 25944, A	
90	551	17.5	551	9	US-09-796-692-9413	Sequence 9413, Ap	
91	551	17.5	551	14	US-10-040-862-9413	Sequence 9413, Ap	
92	551	17.5	551	17	US-10-057-475B-9413	Sequence 9413, Ap	
93	551	17.5	551	17	US-10-154-884B-9413	Sequence 9413, Ap	
94	551	17.5	551	18	US-10-764-324-9413	Sequence 9413, Ap	
c 95	515	16.4	515	16	US-10-029-386-12244	Sequence 12244, A	
96	494	15.7	1223	17	US-10-312-352-46	Sequence 46, Appl	
97	470	15.0	988	18	US-10-363-829-113	Sequence 113, App	
c 98	406.4	12.9	418	9	US-09-796-692-6859	Sequence 6859, Ap	
c 99	406.4	12.9	418	14	US-10-040-862-6859	Sequence 6859, Ap	
c 100	406.4	12.9	418	17	US-10-057-475B-6859	Sequence 6859, Ap	
c 101	406.4	12.9	418	17	US-10-154-884B-6859	Sequence 6859, Ap	
c 102	406.4	12.9	418	18	US-10-764-324-6859	Sequence 6859, Ap	
103	327.8	10.4	400	17	US-10-242-535A-11273	Sequence 11273, A	
104	327.8	10.4	400	17	US-10-085-783A-11273	Sequence 11273, A	
105	263.6	8.4	3766	17	US-10-170-385-92	Sequence 92, Appl	
106	263.6	8.4	3766	17	US-10-295-027-192	Sequence 192, App	
107	263.6	8.4	3766	17	US-10-295-027-994	Sequence 994, App	
108	263.6	8.4	3766	17	US-10-188-832-205	Sequence 205, App	
587	263.6	8.4	3781	15	US-10-241-220-1	Sequence 1, Appli	
604	263.6	8.4	3781	16	US-10-174-587-453	Sequence 453, App	
644	263.6	8.4	3781	16	US-10-013-909A-252	Sequence 252, App	
694	263.6	8.4	3781	18	US-10-872-972-1	Sequence 1, Appli	
695	263.6	8.4	3781	18	US-10-872-991-1	Sequence 1, Appli	
696	255.6	8.1	2514	17	US-10-085-117-72	Sequence 72, Appl	
697	255.6	8.1	3766	17	US-10-085-117-71	Sequence 71, Appl	
698	246.6	7.8	2390	9	US-09-908-193-17	Sequence 17, Appl	
699	237.8	7.6	3293	14	US-10-149-819-25	Sequence 25, Appl	

700	236.6	7.5	2155	13	US-10-003-152-11	Sequence 11, Appl
701	236.6	7.5	2155	14	US-10-002-050-11	Sequence 11, Appl
702	236.6	7.5	2155	14	US-10-002-304-11	Sequence 11, Appl
703	236.6	7.5	2156	13	US-10-003-152-21	Sequence 21, Appl
704	236.6	7.5	2156	14	US-10-002-050-21	Sequence 21, Appl
705	236.6	7.5	2156	14	US-10-002-304-21	Sequence 21, Appl
706	236.6	7.5	2284	13	US-10-003-152-13	Sequence 13, Appl
707	236.6	7.5	2284	14	US-10-002-050-13	Sequence 13, Appl
708	236.6	7.5	2284	14	US-10-002-304-13	Sequence 13, Appl
709	236.6	7.5	2646	17	US-10-312-352-67	Sequence 67, Appl
710	235	7.5	238	9	US-09-796-692-2787	Sequence 2787, Ap
711	235	7.5	238	14	US-10-040-862-2787	Sequence 2787, Ap
712	235	7.5	238	17	US-10-057-475B-2787	Sequence 2787, Ap
713	235	7.5	238	17	US-10-154-884B-2787	Sequence 2787, Ap
714	235	7.5	238	18	US-10-764-324-2787	Sequence 2787, Ap
c 715	235	7.5	1914	17	US-10-190-115-119	Sequence 119, App
716	235	7.5	1914	17	US-10-190-115-121	Sequence 121, App
c 717	235	7.5	1914	17	US-10-190-115-122	Sequence 122, App
718	235	7.5	1914	17	US-10-190-115-124	Sequence 124, App
719	235	7.5	1914	17	US-10-403-676-1	Sequence 1, Appli
720	235	7.5	1914	17	US-10-403-676-7	Sequence 7, Appli
721	235	7.5	1914	17	US-10-403-676-9	Sequence 9, Appli
722	235	7.5	3503	10	US-09-759-130B-336	Sequence 336, App
723	235	7.5	3503	14	US-10-189-123-66	Sequence 66, Appl
724	235	7.5	3503	16	US-10-188-495-66	Sequence 66, Appl
725	235	7.5	3503	18	US-10-741-790-336	Sequence 336, App
726	233.2	7.4	2739	17	US-10-403-676-11	Sequence 11, Appl
727	233.2	7.4	3868	17	US-10-190-115-13	Sequence 13, Appl
728	233.2	7.4	3868	17	US-10-369-072-13	Sequence 13, Appl
729	230	7.3	2433	17	US-10-291-808-24	Sequence 24, Appl
730	225.4	7.2	2558	17	US-10-190-115-15	Sequence 15, Appl
731	225.4	7.2	2558	17	US-10-369-072-15	Sequence 15, Appl
732	225.4	7.2	3112	17	US-10-190-115-17	Sequence 17, Appl
733	225.4	7.2	3112	17	US-10-369-072-17	Sequence 17, Appl
734	225.4	7.2	3112	17	US-10-403-676-5	Sequence 5, Appli
c 735	216.2	6.9	224	9	US-09-954-531-76	Sequence 76, Appl
c 736	216.2	6.9	224	9	US-09-954-531-259	Sequence 259, App
737	200.8	6.4	3360	18	US-10-115-635-8	Sequence 8, Appli
738	193	6.1	2049	17	US-10-403-676-3	Sequence 3, Appli
739	189.6	6.0	8095	9	US-09-989-920-73	Sequence 73, Appl
740	189.6	6.0	8144	11	US-09-989-890-112	Sequence 112, App
c 741	177.2	5.6	1662	13	US-10-027-632-97791	Sequence 97791, A
c 742	177.2	5.6	1662	13	US-10-027-632-100416	Sequence 100416,
c 743	177.2	5.6	1662	13	US-10-027-632-100417	Sequence 100417,
c 744	177.2	5.6	1662	17	US-10-027-632-97791	Sequence 97791, A
c 745	177.2	5.6	1662	17	US-10-027-632-100416	Sequence 100416,
c 746	177.2	5.6	1662	17	US-10-027-632-100417	Sequence 100417,
747	169.8	5.4	2562	17	US-10-085-117-68	Sequence 68, Appl
748	169.8	5.4	2562	17	US-10-085-117-69	Sequence 69, Appl
749	153.4	4.9	2589	17	US-10-052-482-168	Sequence 168, App
750	153.4	4.9	4157	8	US-08-556-422-1	Sequence 1, Appli
751	153.4	4.9	4157	15	US-10-261-049-1	Sequence 1, Appli
752	153.4	4.9	4157	16	US-10-320-769-1	Sequence 1, Appli
753	153.4	4.9	4157	17	US-10-172-118-1275	Sequence 1275, Ap
754	153.4	4.9	4157	17	US-10-342-887-1275	Sequence 1275, Ap
755	153.4	4.9	4157	17	US-10-052-482-167	Sequence 167, App
756	153.4	4.9	6300	16	US-10-252-157-463	Sequence 463, App

757	147	4.7	1024	17	US-10-042-865-3	Sequence 3, Appli
758	143.6	4.6	2586	17	US-10-052-482-165	Sequence 165, App
759	143.6	4.6	2769	17	US-10-052-482-164	Sequence 164, App
760	141	4.5	967	13	US-10-000-512-11	Sequence 11, Appl
761	141	4.5	967	17	US-10-074-566-11	Sequence 11, Appl
762	126	4.0	1801	17	US-10-211-462-164	Sequence 164, App
763	126	4.0	3524	16	US-10-391-413-3	Sequence 3, Appli
764	126	4.0	3524	17	US-10-211-462-166	Sequence 166, App
783	126	4.0	3721	14	US-10-036-160-34	Sequence 34, Appl
913	126	4.0	3721	15	US-10-223-085-267	Sequence 267, App
916	126	4.0	3721	15	US-10-223-084-267	Sequence 267, App
917	126	4.0	3721	15	US-10-223-088-267	Sequence 267, App
918	126	4.0	3721	15	US-10-223-090-267	Sequence 267, App
919	126	4.0	3721	15	US-10-223-087-267	Sequence 267, App
921	126	4.0	3721	15	US-10-223-083-267	Sequence 267, App
922	126	4.0	3721	15	US-10-223-089-267	Sequence 267, App
1083	126	4.0	3721	16	US-10-223-081-267	Sequence 267, App
1099	126	4.0	3721	16	US-10-223-082-267	Sequence 267, App
1210	126	4.0	3721	17	US-10-305-654-267	Sequence 267, App
1219	126	4.0	3721	17	US-10-081-056-267	Sequence 267, App
1232	126	4.0	3721	18	US-10-884-091-34	Sequence 34, Appl
1233	126	4.0	3721	19	US-10-931-886-543	Sequence 543, App
1234	125.4	4.0	3692	16	US-10-391-413-1	Sequence 1, Appli
1235	121.8	3.9	3279	15	US-10-102-524-1855	Sequence 1855, Ap
1236	121.8	3.9	3453	15	US-10-102-524-1854	Sequence 1854, Ap
1237	121.8	3.9	3606	15	US-10-102-524-1853	Sequence 1853, Ap
1238	121.8	3.9	3631	17	US-10-190-115-107	Sequence 107, App
1239	121.8	3.9	3791	18	US-10-775-920-310	Sequence 310, App
1240	121.8	3.9	4233	17	US-10-190-115-105	Sequence 105, App
1241	121.8	3.9	4456	17	US-10-451-010-15	Sequence 15, Appl
1242	121.8	3.9	4559	15	US-10-102-524-1852	Sequence 1852, Ap
1243	121.8	3.9	4559	18	US-10-775-920-308	Sequence 308, App
1252	121.8	3.9	4725	14	US-10-237-535-95	Sequence 95, Appl
1261	121.8	3.9	4725	14	US-10-239-196-95	Sequence 95, Appl
1352	121.8	3.9	4725	18	US-10-643-795A-55	Sequence 55, Appl
1353	121.8	3.9	6408	17	US-10-190-115-11	Sequence 11, Appl
1354	121.8	3.9	6408	17	US-10-369-072-11	Sequence 11, Appl
1355	121.4	3.9	2820	9	US-09-854-845-15	Sequence 15, Appl
1356	121.4	3.9	2865	9	US-09-854-845-13	Sequence 13, Appl
1357	121.4	3.9	3105	9	US-09-854-845-5	Sequence 5, Appli
1358	121.4	3.9	3150	9	US-09-854-845-1	Sequence 1, Appli
1359	121.4	3.9	3237	9	US-09-854-845-7	Sequence 7, Appli
1360	121.4	3.9	3282	9	US-09-854-845-3	Sequence 3, Appli
1361	121.4	3.9	3411	9	US-09-854-845-11	Sequence 11, Appl
1362	121.4	3.9	3456	9	US-09-854-845-9	Sequence 9, Appli
1363	121.4	3.9	4074	9	US-09-854-845-17	Sequence 17, Appl
1364	115.6	3.7	2811	10	US-09-759-130B-303	Sequence 303, App
1365	115.6	3.7	2811	14	US-10-189-123-33	Sequence 33, Appl
1366	115.6	3.7	2811	16	US-10-188-495-33	Sequence 33, Appl
1367	115.6	3.7	2811	18	US-10-741-790-303	Sequence 303, App
1368	114.4	3.6	2675	18	US-10-367-094-91	Sequence 91, Appl
c1369	110	3.5	344	9	US-09-917-800A-651	Sequence 651, App
1370	105.4	3.4	2094	9	US-09-854-845-24	Sequence 24, Appl
1371	105.4	3.4	2517	9	US-09-854-845-28	Sequence 28, Appl
1372	105.4	3.4	2598	9	US-09-854-845-32	Sequence 32, Appl
1373	105.4	3.4	2951	9	US-09-854-845-50	Sequence 50, Appl
1374	102.8	3.3	2337	9	US-09-731-179-3	Sequence 3, Appli

1375	102.4	3.3	2109	9	US-09-854-845-22	Sequence 22, Appl
1376	102.4	3.3	2532	9	US-09-854-845-26	Sequence 26, Appl
1377	102.4	3.3	2575	17	US-10-120-988-40	Sequence 40, Appl
1378	102.4	3.3	2613	9	US-09-854-845-30	Sequence 30, Appl
1379	102	3.2	1327	17	US-10-449-548-21	Sequence 21, Appl
1380	102	3.2	1327	17	US-10-403-676-21	Sequence 21, Appl
1381	102	3.2	1492	17	US-10-449-548-23	Sequence 23, Appl
1382	102	3.2	1492	17	US-10-403-676-23	Sequence 23, Appl
1383	102	3.2	1878	17	US-10-449-548-33	Sequence 33, Appl
1384	102	3.2	1878	17	US-10-403-676-33	Sequence 33, Appl
1385	102	3.2	1890	10	US-09-991-053-29	Sequence 29, Appl
1386	102	3.2	1890	10	US-09-957-187-29	Sequence 29, Appl
1387	102	3.2	1890	10	US-09-957-187-82	Sequence 82, Appl
1388	102	3.2	1908	17	US-10-449-548-35	Sequence 35, Appl
1389	102	3.2	1908	17	US-10-403-676-35	Sequence 35, Appl
1390	102	3.2	1921	17	US-10-449-548-15	Sequence 15, Appl
1391	102	3.2	1921	17	US-10-403-676-15	Sequence 15, Appl
1392	102	3.2	1948	17	US-10-449-548-49	Sequence 49, Appl
1393	102	3.2	1948	17	US-10-403-676-49	Sequence 49, Appl
1394	102	3.2	2583	17	US-10-449-548-51	Sequence 51, Appl
1395	102	3.2	2583	17	US-10-403-676-51	Sequence 51, Appl
1396	102	3.2	2634	17	US-10-449-548-53	Sequence 53, Appl
1397	102	3.2	2634	17	US-10-403-676-53	Sequence 53, Appl
1398	102	3.2	2944	17	US-10-449-548-29	Sequence 29, Appl
1399	102	3.2	2944	17	US-10-403-676-29	Sequence 29, Appl
1400	102	3.2	2995	17	US-10-449-548-19	Sequence 19, Appl
1401	102	3.2	2995	17	US-10-403-676-19	Sequence 19, Appl
1402	102	3.2	3055	17	US-10-449-548-27	Sequence 27, Appl
1403	102	3.2	3055	17	US-10-403-676-27	Sequence 27, Appl
1404	102	3.2	3106	17	US-10-449-548-17	Sequence 17, Appl
1405	102	3.2	3106	17	US-10-403-676-17	Sequence 17, Appl
1406	102	3.2	3165	17	US-10-449-548-47	Sequence 47, Appl
1407	102	3.2	3165	17	US-10-403-676-47	Sequence 47, Appl
1408	102	3.2	3333	10	US-09-991-053-5	Sequence 5, Appli
1409	102	3.2	3333	10	US-09-957-187-5	Sequence 5, Appli
1410	102	3.2	3498	10	US-09-991-053-3	Sequence 3, Appli
1411	102	3.2	3498	10	US-09-957-187-3	Sequence 3, Appli
1412	102	3.2	3498	17	US-10-449-548-31	Sequence 31, Appl
1413	102	3.2	3498	17	US-10-403-676-31	Sequence 31, Appl
1414	102	3.2	4250	10	US-09-957-187-84	Sequence 84, Appl
1415	102	3.2	4250	16	US-10-393-892-30	Sequence 30, Appl
1416	102	3.2	4250	16	US-10-394-382-30	Sequence 30, Appl
1417	102	3.2	4250	17	US-10-449-548-13	Sequence 13, Appl
1418	102	3.2	4250	17	US-10-403-676-13	Sequence 13, Appl
1419	102	3.2	4250	18	US-10-723-860-2800	Sequence 2800, Ap
1420	102	3.2	4280	17	US-10-120-988-330	Sequence 330, App
1421	102	3.2	4612	18	US-10-367-094-94	Sequence 94, Appl
1422	102	3.2	7281	18	US-10-723-860-5596	Sequence 5596, Ap
1423	100.4	3.2	1438	17	US-10-449-548-25	Sequence 25, Appl
1424	100.4	3.2	1438	17	US-10-403-676-25	Sequence 25, Appl
1425	100.4	3.2	2113	17	US-10-449-548-55	Sequence 55, Appl
1426	100.4	3.2	2113	17	US-10-403-676-55	Sequence 55, Appl
1427	100.4	3.2	3983	17	US-10-449-548-45	Sequence 45, Appl
1428	100.4	3.2	3983	17	US-10-403-676-45	Sequence 45, Appl
1429	99	3.1	2893	10	US-09-808-665A-1	Sequence 1, Appli
1430	99	3.1	2894	10	US-09-808-665A-3	Sequence 3, Appli
1431	98.6	3.1	1797	9	US-09-854-845-40	Sequence 40, Appl

1432	98.6	3.1	2220	9	US-09-854-845-44	Sequence 44, Appl
1433	98.6	3.1	2301	9	US-09-854-845-48	Sequence 48, Appl
1434	98.6	3.1	2790	14	US-10-300-834-5	Sequence 5, Appli
1435	98.6	3.1	3432	14	US-10-300-834-4	Sequence 4, Appli
1436	95.6	3.0	1812	9	US-09-854-845-38	Sequence 38, Appl
1437	95.6	3.0	2235	9	US-09-854-845-42	Sequence 42, Appl
1438	95.6	3.0	2316	9	US-09-854-845-46	Sequence 46, Appl
1439	92.8	3.0	729	10	US-09-759-130B-304	Sequence 304, App
1440	92.8	3.0	729	14	US-10-189-123-34	Sequence 34, Appl
1441	92.8	3.0	729	16	US-10-188-495-34	Sequence 34, Appl
1442	92.8	3.0	729	18	US-10-741-790-304	Sequence 304, App
1443	89.8	2.9	2787	14	US-10-300-834-2	Sequence 2, Appli
1444	89.8	2.9	3195	14	US-10-300-834-1	Sequence 1, Appli
1445	89.4	2.8	4003	18	US-10-723-860-5060	Sequence 5060, Ap
1446	83	2.6	2919	15	US-10-262-538-11	Sequence 11, Appl
1447	83	2.6	2919	16	US-10-285-351B-2	Sequence 2, Appli
1448	83	2.6	2919	18	US-10-669-176-11	Sequence 11, Appl
1449	79.6	2.5	2349	9	US-09-813-290-3	Sequence 3, Appli
1450	79.6	2.5	2628	9	US-09-813-290-1	Sequence 1, Appli
1451	79.6	2.5	3568	9	US-09-813-290-5	Sequence 5, Appli
1452	79.6	2.5	4700	17	US-10-172-118-1824	Sequence 1824, Ap
1453	79.6	2.5	4700	17	US-10-342-887-1824	Sequence 1824, Ap
1454	79.6	2.5	4700	18	US-10-723-860-2944	Sequence 2944, Ap
1455	79.6	2.5	4936	18	US-10-723-860-6994	Sequence 6994, Ap
1456	78.6	2.5	3560	16	US-10-067-632-59	Sequence 59, Appl
1457	78.2	2.5	1923	18	US-10-312-281-12	Sequence 12, Appl
1458	78.2	2.5	1923	18	US-10-461-791-12	Sequence 12, Appl
1459	78.2	2.5	3261	18	US-10-312-281-5	Sequence 5, Appli
1460	78.2	2.5	3261	18	US-10-461-791-5	Sequence 5, Appli
1461	78.2	2.5	3694	18	US-10-312-281-3	Sequence 3, Appli
1462	78.2	2.5	3694	18	US-10-461-791-3	Sequence 3, Appli
1463	78	2.5	1491	9	US-09-854-845-20	Sequence 20, Appl
1464	76.6	2.4	1896	17	US-10-016-248-9	Sequence 9, Appli
1465	76.6	2.4	2191	17	US-10-016-248-13	Sequence 13, Appl
1466	76.6	2.4	2359	17	US-10-016-248-17	Sequence 17, Appl
1467	76.6	2.4	3196	17	US-10-016-248-15	Sequence 15, Appl
1468	76.6	2.4	3205	17	US-10-016-248-11	Sequence 11, Appl
1469	76.6	2.4	3364	17	US-10-016-248-19	Sequence 19, Appl
1470	76.6	2.4	4234	17	US-10-451-010-12	Sequence 12, Appl
1471	76.2	2.4	2340	9	US-09-731-179-1	Sequence 1, Appli
1472	71.4	2.3	8056	18	US-10-723-860-4273	Sequence 4273, Ap
1473	71.4	2.3	8214	18	US-10-723-860-8119	Sequence 8119, Ap
1474	71.2	2.3	928	14	US-10-188-246-13	Sequence 13, Appl
1475	71.2	2.3	1194	9	US-09-854-845-36	Sequence 36, Appl
1476	69.8	2.2	2670	16	US-10-067-632-61	Sequence 61, Appl
1477	68	2.2	777	14	US-10-188-246-15	Sequence 15, Appl
1478	66.6	2.1	1755	9	US-09-978-249-4	Sequence 4, Appli
1479	65.2	2.1	648	9	US-09-854-845-18	Sequence 18, Appl
1480	63.8	2.0	2530	14	US-10-097-340-283	Sequence 283, App
1481	63.8	2.0	2530	15	US-10-262-538-9	Sequence 9, Appli
1482	63.8	2.0	2530	18	US-10-669-176-9	Sequence 9, Appli
1483	63.8	2.0	2530	18	US-10-723-860-2569	Sequence 2569, Ap
1484	63.8	2.0	2601	16	US-10-067-632-53	Sequence 53, Appl
1485	63.8	2.0	2709	9	US-09-774-490-1	Sequence 1, Appli
1486	63.8	2.0	2848	16	US-10-247-671-83	Sequence 83, Appl
1487	63.8	2.0	3023	18	US-10-723-860-6714	Sequence 6714, Ap
1488	62	2.0	2854	16	US-10-067-632-57	Sequence 57, Appl

c1489	60.6	1.9	828	17	US-10-276-774-37	Sequence 37, Appl
1490	60	1.9	60	10	US-09-908-975-15844	Sequence 15844, A
1491	58.4	1.9	351	9	US-09-854-845-34	Sequence 34, Appl
1492	58	1.8	39780	17	US-10-052-482-163	Sequence 163, App
1493	57.6	1.8	3552	17	US-10-231-956A-437	Sequence 437, App
1494	57.6	1.8	3552	18	US-10-775-169-25	Sequence 25, Appl
1495	57.2	1.8	495	10	US-09-918-995-51	Sequence 51, Appl
1496	56.6	1.8	48244	17	US-10-052-482-166	Sequence 166, App
1497	55.6	1.8	273	11	US-09-864-408A-5889	Sequence 5889, Ap
1498	53	1.7	64921	17	US-10-085-117-70	Sequence 70, Appl
1499	52.6	1.7	2898	13	US-10-144-031-2	Sequence 2, Appli
1500	52.4	1.7	445	9	US-09-764-853-385	Sequence 385, App

Search completed: February 15, 2005, 02:59:35
Job time : 1705 secs